

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 2, 2001, 15:09:55 ; Search time 19.72 Seconds
(without alignments)
626.129 Million cell updates/sec

Title: US-09-602-597-4

Perfect score: 1101
Sequence: 1 MAFPSKSTRTSSPAQGA.....GSOSRVTLQASGALRGVSP 216

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A_Geneseq_0401:*

1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT:*

2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT:*

3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT:*

4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT:*

5: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT:*

6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT:*

7: /SID56/gcgdata/geneseq/geneseq/AA1986.DAT:*

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9: /SID56/gcgdata/geneseq/geneseq/AA1988.DAT:*

10: /SID56/gcgdata/geneseq/geneseq/AA1989.DAT:*

11: /SID56/gcgdata/geneseq/geneseq/AA1990.DAT:*

12: /SID56/gcgdata/geneseq/geneseq/AA1991.DAT:*

13: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT:*

14: /SID56/gcgdata/geneseq/geneseq/AA1993.DAT:*

15: /SID56/gcgdata/geneseq/geneseq/AA1994.DAT:*

16: /SID56/gcgdata/geneseq/geneseq/AA1995.DAT:*

17: /SID56/gcgdata/geneseq/geneseq/AA1996.DAT:*

18: /SID56/gcgdata/geneseq/geneseq/AA1997.DAT:*

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21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT:*

22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	930	84.5	182	21	Y70458 Human membrane cha
2	848	77.0	182	17	R99799 NTR1-11 nerve prot
3	580	52.7	113	21	B34711 Human secreted pro
4	325	29.5	173	21	V53643 A bone marrow secr
5	307	27.9	153	19	W52117 Human proteolipid
6	191	17.3	101	20	Y41391 Human secreted pro
7	148.5	13.5	169	21	B56719 Human prostatic can
8	147.5	13.4	265	22	B49502 Clone HYASC03. HO
9	144	13.1	153	9	P81879 Sequence of full-1
10	144	13.1	153	9	P80929 Sequence of human
11	137.5	12.5	276	21	B42947 Human ORFX ORF2711

12	137.5	12.5	322	21	B15549 Human immune syste
13	137.5	12.5	322	21	B19729 Human SECC Clone 4
14	137.5	12.5	322	21	Y99349 Human PRO110 (UNG
15	137	12.4	254	21	B56922 Human prostate can
16	127.5	11.6	254	21	B24446 Human secreted pro
17	127.5	11.6	299	21	B23042 Human myeloid upre
18	115	10.4	175	21	B29644 Human membrane-ass
19	110.5	10.0	136	20	Y33297 Human membrane spa
20	94	8.5	34	20	Y41565 Fragment of human
21	92.5	8.4	125	21	B42930 Human ORFX ORF2694
22	91	8.3	421	20	Y35514 Chlamydia pneumoni
23	86.5	7.9	400	14	R32501 Beta-adrenergic re
24	85	7.7	1088	21	B42406 Human ORFX ORF2170
25	84.5	7.7	246	21	B29615 Cat flea HPT NMDA
26	82	7.4	456	19	W69555 Human equilibrativ
27	82	7.4	456	21	B15520 Human ENTI protein
28	81.5	7.4	388	13	R25698 Murine adrenergic
29	81.5	7.4	400	15	R54992 Murine beta-3 adre
30	81	7.4	230	21	G19552 Arabidopsis thalia
31	81	7.4	237	21	G19551 Arabidopsis thalia
32	81	7.4	255	21	B19414 An aromatic class
33	81	7.4	272	21	G19550 Arabidopsis thalia
34	81	7.4	553	20	Y38796 Neisseria meningit
35	80.5	7.3	359	21	Y69485 Amino acid sequenc
36	80	7.3	232	21	G32159 Arabidopsis thalia
37	80	7.3	239	21	G32158 Arabidopsis thalia
38	80	7.3	280	21	G32157 Arabidopsis thalia
39	79.5	7.2	405	19	W44933 Canine beta-3 adre
40	79.5	7.2	476	18	W24089 Balanus amphitrite
41	79	7.2	306	21	B43004 Human ORFX ORF2768
42	79	7.2	306	22	B49652 Human SEC4 protein
43	79	7.2	394	21	Y81725 Streptococcus pneu
44	79	7.2	1670	21	G31673 Arabidopsis thalia
45	79	7.2	1753	21	G31672 Arabidopsis thalia

ALIGNMENTS

RESULT	ID	Y70458	standard; Protein; 182 AA.
1	Y70458		
XX	XX	Y70458:	
AC	XX	21-JUN-2000 (first entry)	
DT	XX		
XX	XX	Human membrane channel protein-8 (MECHP-8).	
DE	XX		
XX	XX	Membrane channel protein-8; MECHP-8; diagnosis; treatment; lymphoma;	
KW	KW	cell proliferative disorder; bursitis; atherosclerosis; cancer; sarcoma;	
KW	KW	inflammatory disorder; AIDS; Addison's disease; cystic fibrosis; asthma;	
KW	KW	diabetes mellitus; osmoregulatory disorder; diarrhoea; renal failure;	
KW	KW	muscular disorder; myocarditis; Duchenne's muscular dystrophy; nocturnal;	
KW	KW	cardiovascular disorder; hypertension; bronchitis; vasculitis; candida;	
KW	KW	neurological disorder; Alzheimer's disease; Parkinson's disease; human;	
KW	KW	Huntington's disease; antiarteriosclerotic; hepatotropic; cystostatic;	
KW	KW	anti-HIV; antitumoric; neuroprotective; immunomodulatory; antidiabetic;	
KW	KW	hypotensive; vasotrophic; antisthmatic; antiinflammatory; antidepressant;	
KW	KW	anticonvulsant; thrombolytic; antiParkinsonian; immunostimulant.	
OS	XX	Homo sapiens.	
XX	XX		
XX	XX	Key	Location/Qualifiers
FT	FT	Modified-site	9
FT	FT	Modified-site	/note- "Phosphorylation site"
FT	FT	Modified-site	130
FT	FT	Modified-site	/note- "Phosphorylation site"
FT	FT	Modified-site	108
FT	FT	Modified-site	/note- "Glycosylation site"
FT	FT	Domain	36..55
FT	FT	Domain	/label- Transmembrane_domain
FT	FT	Domain	65..84

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FT      Domain /label-Transmembrane_domain
FT      103..130
XX      /label-Transmembrane_domain
XX      W0200012711-A2.
XX      09-MAR-2000.
XX      02-SEP-1999; 99WO-US20468.
XX      02-SEP-1998; 98US-0145815.
XX      12-NOV-1998; 98US-0191283.
XX      09-DEC-1998; 98US-0208821.
XX      26-JAN-1999; 99US-0237506.
XX      10-FEB-1999; 99US-0247891.
XX      (INCYTE PHARM INC.
XX      Au-Young J, Bandman O, Tang YT, Reddy R, Hillman JL, Yue H;
XX      Lal P, Corley NC, Guegler KJ, Gorgone G, Baughn MR, Azimzal Y;
XX      WPI; 2000-256643/22.
XX      N-PSDB; 251624.
XX      Novel human membrane channel protein and polynucleotide useful for
XX      diagnosing and treating cell proliferative, inflammatory, secretory,
XX      osmoregulatory, muscular, cardiovascular and neurological disorders
XX      Claim 1; Page 107; 140pp; English.
XX      The present sequence is the human membrane channel protein-8 (MECHP-8),
XX      which is expressed in nervous and gastrointestinal tissues. Anti-MECHP
XX      antibodies can be used as therapeutic antagonists and reagents for
XX      diagnosis and monitoring diseases. MECHP cDNA can be used for diagnosis
XX      of MECHP-related diseases and gene mapping. MECHP can be used for
XX      treatment of cell proliferative disorders such as buritis and
XX      atherosclerosis, cancers like lymphoma and sarcoma, inflammatory
XX      disorders like AIDS and Addison's disease, transport/secretory disorders
XX      like cystic fibrosis and diabetes mellitus, osmoregulatory disorders like
XX      diarrhoea and renal failure, muscular disorders like myocardiitis and
XX      Duchenne's muscular dystrophy, cardiovascular disorders like hypertension
XX      and vasculitis, congenital lung anomalies like bronchitis and asthma and
XX      neurological disorders like Alzheimer's disease, Parkinson's disease and
XX      Huntington's disease.
XX      Sequence 182 AA;
XX      SQ
XX      Query Match 84.5%; Score 930; DB 21; Length 182;
XX      Best Local Similarity 100.0%; Pred. No. 6.1e-98;
XX      Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      QY 1 MAEPPSKVSTRTSSPAOGAASVSAALRPDGLFVRSRLGALMLQVLVGLVWMLIADTPY 60
XX      Db 1 maeppskvstrtsspaogaaesvsaalrpdglfvrslgalmllqvlvllwmladtpy 60
XX      QY 61 HLYPAYGWVWFVAVFLVTLVIVLFNLFLFQHLHKLTVMPVPLVMTNISAIVLYITAFI 120
XX      Db 61 hlypaygwvmfvaflvltvlvlnlflfqlhmklymvpplvmtlnisatvlyitafi 120
XX      QY 121 ACSAAVDLTSIRGTRPYNORAAAFACLVMIAYGVSAFVSQYAMRGVSNAAATSQMAG 180
XX      Db 121 acaaaavdltsirgtrpyngtraaafacvlmlyaygsafvsqaygwsgnaatsqmag 180
XX      QY 181 YA 182
XX      Db 181 ya 182
XX      RESULT 2
XX      R99799 ID R99799 standard; Protein; 182 AA.
XX      XX

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AC      R99799;
XX      02-JAN-1997 (first entry)
XX      NTII-11 nerve protein, facilitates regeneration of nerve cells.
XX      DE
XX      Probe: central nervous system; peripheral nervous system; CNS; PNS;
XX      axon; neurone; neuronal cells; glial cells; Schwann cells; trauma;
XX      pathology; regeneration; MS2; metalloprotease.
XX      KW
XX      Homo sapiens.
XX      OS
XX      MO9617865-A2.
XX      PD 13-JUN-1996.
XX      PF 05-DEC-1995; 95WO-EP04777.
XX      PR 27-JAN-1995; 95DE-4002525.
XX      PR 05-DEC-1994; 94DE-4443159.
XX      PA (BOE ) BOEHRINGER MANNHEIM GMBH.
XX      PI Gillen C, Gleichmann M, Mueller H;
XX      DR WPI; 1996-287114/29.
XX      DR N-PSDB; T34592.
XX      PT Nucleic acids associated with damaged or regenerating nerve cells
XX      for diagnostic or therapeutic use.
XX      PS Claim 4; Page 45-46; 54pp; German.
XX      CC Nucleic acids described in T34587-T34616 are useful as probes for
XX      detecting traumatic and pathological changes in the peripheral
XX      nervous system. They may also be used to identify hybridising
XX      sequences from an ischial nerve cDNA library, these sequences encode
XX      proteins expressed in damaged and/or regenerating nerve cells. They
XX      can be used to transfect cells which then express the protein which
XX      can then be harvested and studied. The nucleic acids are preferably
XX      selected from NTII-11 which corresponds to plasmolipin cDNA with a
XX      234 bp N-terminal extension and is expressed in glial cells of the
XX      central nervous system and Schwann cells of the peripheral nervous
XX      system; NTII-1, which codes for this protein having 798 homology
XX      with human CDC4L in three domains and may be involved in regulating
XX      Schwann cell growth as well as being therapeutically useful for
XX      regenerating nerve cells; and CRII-7 which codes for a protein
XX      which is similar to the macrophage-specific cysteine-rich mouse
XX      protein MS2 and a metalloprotease and which inhibits interaction
XX      between Schwann cells and the extracellular matrix and is useful
XX      for the therapy of nerve damage by facilitating regeneration of
XX      damaged axons.
XX      SQ
XX      Sequence 182 AA;
XX      SQ
XX      Query Match 77.0%; Score 848; DB 17; Length 182;
XX      Best Local Similarity 88.5%; Pred. No. 1.3e-88;
XX      Matches 161; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
XX      QY 1 MAEPPSKVSTRTSSPAOGAASVSAALRPDGLFVRSRLGALMLQVLVGLVWMLIADTPY 60
XX      Db 1 maeppskvstrtsspaogaaesvsaalrpdglfvrslgalmllqvlvllwmladtpy 60
XX      QY 61 HLYPAYGWVWFVAVFLVTLVIVLFNLFLFQHLHKLTVMPVPLVMTNISAIVLYITAFI 120
XX      Db 61 hlypaygwvmfvaflvltvlvlnlflfqlhmklymvpplvmtlnisatvlyitafv 120
XX      QY 121 ACSAAVDLTSIRGTRPYNORAAAFACLVMIAYGVSAFVSQYAMRGVSNAAATSQMAG 180
XX      Db 121 acaaaavdltsirgtrpyngtraaafacvlmlyaygsafvsqaygwsgnaatsqmag 180
XX      QY 181 YA 182
XX      Db 181 ya 182
XX      RESULT 2
XX      R99799 ID R99799 standard; Protein; 182 AA.
XX      XX

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Db      181 ys 182

RESULT 3
B34711 ID B34711 standard; Protein: 113 AA.
XX
XX B34711;
XX
XX 26-JAN-2001 (first entry)
XX
DE      Human secreted protein encoded by DNA clone v06 1.
XX
XX Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer;
XX systemic lupus erythematosus; rheumatoid arthritis; anaemia; stroke;
XX haematopoietic regulation; tissue regrowth; wound healing; haemophilia;
XX Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer;
XX contraceptive; infection; growth inhibition; hyperproliferative disorder;
XX psoriasis.
XX
XX Homo sapiens.
XX
XX WO200055375-A1.
XX
XX 21-SEP-2000.
XX
XX 17-MAR-2000; 2000WO-US07285.
XX
XX 17-MAR-1999; 99US-0124808.
XX 17-MAR-1999; 99US-0124916.
XX 17-AUG-1999; 99US-0149639.
XX 01-OCT-1999; 99US-0157247.
XX 29-NOV-1999; 99US-0167824.
XX 15-FEB-2000; 2000US-0182711.
XX
XX (ALPH-) ALPHAGENE INC.
XX
XX Valenzuela D, Yuan O, Hoffman H, Hall J, Rapleyko P;
XX
XX WPI: 2000-638211/61.
XX
XX N-PSDB; C59812.
XX
XX Novel proteins and polypeptides useful for the treatment of e.g
XX multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis,
XX cancer, Alzheimer's disease, Parkinson's disease, stroke, anemia and
XX ulcers
XX
XX Claim 58; Page 419; 493pp; English.
XX
XX This invention relates to 59 human secreted proteins and the nucleotide
XX sequences encoding them. Sequences C59788-C59846 and B34687-B34745
XX represent the proteins and their encoding nucleotide sequences, and
XX sequences B34746-B34771 represent fragments of the proteins. Probes for
XX the DNA sequences are represented by sequences C59847-C59896. The
XX proteins exhibit neuroprotective, dermatological, immunosuppressive,
XX antiinflammatory, antianaemic, nootropic, antiparkinsonian,
XX cerebroprotective, haemostatic, vulnerary, cytostatic, antiproliferative,
XX antibacterial, virucide, and fungicide activity. The proteins and
XX nucleotide sequences are useful as nutritional sources or supplements
XX and in research. The proteins are useful for treating immune deficiency
XX and disorders, which may be genetic or resulting from infections,
XX autoimmune disorders such as multiple sclerosis, systemic lupus
XX erythematosus, rheumatoid arthritis, and for treating myeloid or lymphoid
XX cell deficiencies such as anaemias by regulating haematopoiesis. The
XX proteins are also useful in compositions for bone, cartilage, tendon,
XX ligament and/or nerve tissue growth or regeneration, for wound healing,
XX tissue repair and replacement and in the treatment of wounds, incisions
XX and ulcers. Other uses include in the treatment of central and peripheral
XX nervous system and neuropathies such as Alzheimer's and Parkinson's
XX diseases and Shy-Drager syndrome, and mechanical and traumatic disorders,
XX such as spinal cord disorders, head trauma and stroke. The proteins may
XX also be used as a contraceptive, and for treating coagulation disorders

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CC such as haemophilias. The protein and nucleotide sequences with cadherin
CC activity are useful for treating cancer. Other uses for the protein
CC include for inhibiting the growth, infection or function of, or killing,
CC infectious agents such as bacteria, virus, fungi and other parasites, for
CC effecting bodily characteristics such as height, weight, hair colour,
CC effecting biorhythms or cardiac cycles or rhythms, effecting
CC metabolism, catabolism, anabolism, processing, utilization, storage or
CC elimination of dietary fat, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors, effecting behavioural characteristics, providing
CC analgesic effects and for treating hyperproliferative disorders such as
CC psoriasis.
XX
XX Sequence 113 AA.
XX
XX Query Match 52.7%; Score 580; DB 21; Length 113;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-58;
XX Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 70 MEYAVFLMLVTVLENYLFOLHMKLYMPWPIVLMIFNISATVLYITAPICSAADVLT 129
XX 1 mfvavflwlvltvlylfnlylfqlhmklymwpwplvmlfnlsatvlyltafacsaaavdl 60
XX
XX Db 130 SLRGTRPYNQRAASFPAQLYMTAVGVSAFVSQARQVGSNNAATSGMAGTA 182
XX 61 slrgtrpyngraasfpaqlymtavgvsaifvsqarqvgvsnnaatsqmagyta 113
XX
XX RESULT 4
XX Y53643
XX ID Y53643 standard; Protein: 173 AA.
XX
XX AC Y53643;
XX
XX 22-FEB-2000 (first entry)
XX
XX A bone marrow secreted protein designated BMS6.
XX
XX DE Bone marrow secreted protein; bone marrow stromal cell; cytokine;
XX cell proliferation; cell differentiation; hematopoiesis; anaemia;
XX myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;
XX erythroid progenitor cell; colony stimulating factor; granulocyte;
XX monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;
XX platelet disorder; thrombocytopenia; hematopoietic stem cell;
XX stem cell disorder; aplastic anaemia; bone differentiation;
XX paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;
XX ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;
XX bone fracture; cartilage damage; artificial joint.
XX
XX Homo sapiens.
XX
XX OS
XX MO9933979-A2.
XX
XX 08-JUL-1999.
XX
XX 18-DEC-1998; 98WO-US27008.
XX
XX 30-DEC-1997; 97US-0068958.
XX 24-SEP-1998; 98US-0101603.
XX 30-SEP-1998; 98US-0102540.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Lin H, Cao L;
XX
XX WPI: 2000-038344/03.
XX
XX N-PSDB; Z36249.
XX
XX New isolated human polynucleotide and secreted proteins can induce
XX production of other cytokines in certain cell populations -
XX
XX Claim 2; Page 119; 120pp; English.
XX

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Y53622-43 represent bone marrow secreted proteins of human bone marrow stromal cells. The proteins can exhibit cytokine, cell proliferation, or cell differentiation activity (either inducing or inhibiting). They can be used to support colony forming cells or factor-dependent cell lines, to regulate hematopoiesis, and to treat myeloid or lymphoid cell deficiencies. In addition, they may be used to support the growth and proliferation of erythroid progenitor cells, and to treat various anaemias. They can have colony stimulating factor (CSF) activity and can be used to support the growth and proliferation of myeloid cells such as granulocytes, monocytes or macrophages, to prevent or treat myelo-suppression, to support the growth and proliferation of megakaryocytes and platelets, thereby allowing prevention or treatment of platelet disorders such as thrombocytopenia, to support the growth and proliferation of hematopoietic stem cells, either in place of or in conjunction with platelet transfusions, to treat stem cell disorders, such as aplastic anemia and paroxysmal nocturnal hemoglobinuria, or to repopulate the stem cell compartment after irradiation or chemotherapy. They can be used for growth or differentiation of bone, cartilage, tendon, ligament, or nerve tissue, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers, to induce cartilage and/or bone growth in circumstances where bone is not normally formed and thus have an application in healing bone fractures and cartilage damage or defects, prophylactic use in fracture reduction and also in the improved fixation of artificial joints.

Sequence 173 AA;

Query Match 29.5%; Score 325; DB 21; Length 173;
Best Local Similarity 43.8%; Pred. No. 4e+29;
Matches 71; Conservative 29; Mismatches 54; Indels 8; Gaps 2;

OY 8 VSTRSPAGAEASVSLRPLGVRSRRLGALMLDLVGLVWALADPPIHRYXG 67
DB 12 VLTSSAENFSSSSSFAYGRELITLPIGLVAELVGLVWLTLAGTEYFVPafg 71
OY 68 WMEFAVFLMTVTLVFLNLYLFQLHMKLYMPVPLVIMFINSALVITFIACSAVD 127
DB 72 WMEFAVFLMTVTLVFLNLYLFQLHMKLYMPVPLVIMFINSALVITFIACSAVD 127
OY 128 LTSL---RGTREYNORALASFPACIMTAYGVSAFSTYOAMR 166
DB 127 assveperdslnfnasassffafvltcygntfyfsfiawr 168

RESULT 5

ID W52117 standard; Protein; 153 AA.

AC W52117;

DT 07-JUL-1998 (first entry)

DE Human proteolipid (PLHu) protein.

KM Human proteolipid; PLHu; exocytosis; membrane trafficking;

KW rat plasmolipin; chemokine; inflammation.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 20..40 "Transmembrane domain 1"

FT Domain 50..72 "Transmembrane domain 1"

FT Domain 84..108 "Transmembrane domain 2"

FT Domain 127..147 "Transmembrane domain 3"

FT Domain 127..147 "Transmembrane domain 4"

PN W09804691-A1.

PD 05-FEB-1998.

XX 21-JUL-1997; 97WO-US12734.
XX 26-JUL-1996; 96US-0695736.
XX (INCY-) INCYTE PHARM INC.
PI Au-Young J, Bandman O, Goll SK, Hillman JL;
XX WPI: 1998-130683/12.
DR N-PSDB: V17143.
PT Human proteolipid PLHu - used to accelerate diagnosis and proper treatment of diseases and conditions associated with abnormal membrane trafficking
PS Claim 1; Fig 1A-1B; 53pp; English.
XX The present sequence is of a human proteolipid (PLHu) protein which was expressed by PLHu CDNA of the current invention. A partial sequence of PLHu CDNA was initially isolated as incyte clone 640699 derived from a human breast CDNA library. Homology of PLHu protein to rat plasmolipin indicates its involvement in exocytosis. Exocytosis facilitated by PLHu may influence membrane trafficking within the cell and could affect the release of chemokines involved in cell migration, proteases which are active in inflammation or other similar activities involving endothelial cells, fibroblasts, etc. The invention also claims for antibodies against PLHu which can be used for e.g. in diagnostic tests to accelerate diagnosis and proper treatment of conditions associated with abnormal membrane trafficking.

Sequence 153 AA;

Query Match 27.9%; Score 307; DB 19; Length 153;
Best Local Similarity 44.6%; Pred. No. 3.8e-27;
Matches 66; Conservative 27; Mismatches 47; Indels 8; Gaps 2;

OY 22 SVSLRPLGVRSRRLGALMLDLVGLVWALADPPIHRYXG 81
DB 6 ssssfaygrelitlplglvaelvglvwltagteyfpvagymfvaavfylvltv 65

OY 82 VLFNLYLFQLHMKLYMPVPLVIMFINSALVITFIACSAVDLTSL---RGTREYN 138
DB 66 fflilylmtcytrlpqvpwtvgjcfngsatsvlylsa-----avdassvperdslnfn 120

OY 139 ORAAAFACLMYMIAYGVSAFSTYOAMR 166
DB 121 swaassffafvltcygntfyfsfiawr 148

RESULT 6

ID Y41391 standard; Protein; 101 AA.

AC Y41391;

DT 02-DEC-1999 (first entry)

DE Human secreted protein encoded by gene 84 clone HSAVN65.

KM Human; secreted protein; fusion protein; gene therapy; protein therapy;

KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;

KW developmental abnormality; foetal deficiency; blood; allergy; renal;

KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;

KW inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;

KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;

KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;

KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

OS Homo sapiens.

PN W09947540-A1.

XX 23-SEP-1999.
PD
XX
PF 18-MAR-1999; 99W0-US05804.
XX
PR 19-MAR-1998; 98US-0078563.
PR 19-MAR-1998; 98US-0078566.
PR 19-MAR-1998; 98US-0078573.
PR 19-MAR-1998; 98US-0078574.
PR 19-MAR-1998; 98US-0078576.
PR 19-MAR-1998; 98US-0078577.
PR 19-MAR-1998; 98US-0078578.
PR 19-MAR-1998; 98US-0078579.
PR 19-MAR-1998; 98US-0078581.
PR 01-APR-1998; 98US-0080312.
PR 01-APR-1998; 98US-0080313.
PR 01-APR-1998; 98US-0080314.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
PI Ruben SM, Ni J, Rosen CA, Yu G, Young PE, Feng P, Soppet DR;
PI Wei Y, Endress GA, Duan RD, Kyaw H, Ebner R, Lafleur DW;
PI Olsen HS, Shi Y, Moore PA;
XX
XX MPI: 1999-562050/47.
DR N-PSDB; Z24894.
XX
XX New isolated human genes, useful for diagnosis and treatment of e.g.
PT cancers, neurological disorders, immune diseases, inflammation or blood
PT disorders -
XX
XX Claim 11; Page 407408; 484pp; English.
PS
XX This sequence represents a secreted human protein encoded by the gene
CC clone detailed in the descriptor line. The gene can be used to generate
CC fusion proteins by linking to the gene to a human immunoglobulin Fc
CC portion (e.g. Z24802) for increasing the stability of the fused protein
CC as compared to the human protein only.
CC The invention relates to 95 novel genes and their fragments (nucleic
CC acid sequences: Z24811-Z24907; amino acid sequences Y41308-Y41404) which
CC are useful for preventing, treating or ameliorating medical conditions
CC e.g. by protein or gene therapy. Also, pathological conditions can be
CC diagnosed by determining the amount of the new polypeptides in a sample
CC or by determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 95 polynucleotides, based on
CC which tissues they are most highly expressed in (see Z24811 for described
CC uses).
XX
XX Sequence 101 AA;
SQ

Query Match 17.3%; Score 191; DB 20; Length 101;
Best Local Similarity 41.0%; Pred. No. 3.4e-14;
Matches 41; Conservative 20; Mismatches 31; Indels 8; Gaps 2;
QY 70 MRYAVFLMTVLTLENYLFQLMKLYWPPWPLVIMFINSATVLYTAFACSAADVLT 129
DB 1 MRYAVFLMTVLTLENYLFQLMKLYWPPWPLVIMFINSATVLYTAFACSAADVLT 129
QY 130 SL---RGTRPYNORAAAFACIYMTAYGVSAFESIOAMR 166
DB 56 svspkdsnfnswassffatvlcygnutyfsixavr 95

RESULT 7
B56719
ID B56719 standard; Protein; 169 AA.
XX
AC B56719;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen protein sequence SEQ ID NO:1297.

XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease.
XX
OS Homo sapiens.
XX WO20005174-A1.
XX
XX 21-SEP-2000.
PD
XX 08-MAR-2000; 2000W0-US05988.
PF
XX 12-MAR-1999; 99US-0124270.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
XX Rosen CA, Ruben SM;
XX
XX MPI: 2000-587513/55.
DR N-PSDB; F15922.
XX
XX Prostate cancer associated gene sequences, referred to as prostate
PT cancer antigens, useful for treatment, prevention, and diagnosis of
PT disorders such as prostate cancer -
XX
XX Claim 11; Page 1718; 2338pp; English.
PS
XX F15566 to F16505 encode the human prostate cancer associated proteins,
CC called prostate cancer antigens, given in B56363 to B57302. The prostate
CC cancer antigens can have neuroprotective, cytostatic, cardioactive,
CC immunomodulatory, muscular, vulnary, gastrointestinal, nephrotropic,
CC antiinfective, gynaecological and antibacterial activities, and can be
CC used in gene therapy. The prostate cancer antigen polynucleotides may be
CC used for detection of prostate cancer. Chromosome identification, as
CC chromosome markers, and for numerous other diagnostic or research
CC purposes. The prostate cancer antigens may be used to treat disorders
CC such as neural, immune, muscular, reproductive, gastrointestinal,
CC pulmonary, cardiovascular, renal, and proliferative disorders, wounds,
CC and infectious diseases. F16506 to F16514 to B57303 represent sequences
CC used in the exemplification of the present invention.
XX
XX Sequence 169 AA;
SQ

Query Match 13.5%; Score 148.5; DB 21; Length 169;
Best Local Similarity 30.2%; Pred. No. 4.7e-09;
Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;
QY 39 ALMLQVLVGLVYMALADPPHYLP-AYGWWVFVFLVYVFNLYLQHLKLM 97
DB 45 ALFLPILFGLVWVAVAT-hivppllgvwmvvaltflslmlllgfgr--f 101.
QY 98 VPPVLYIMFINSATVLYT-ATFACSAADVLTSLGTRPYNORAAAFACIYMTAYGV 156
DB 102 esvrvldslghnctglllymsaavlyghatlvseklldprrlylnsaasffatlllyl 161
QY 157 SAFESY 162
DB 162 hafsly 167

RESULT 8
B49502
ID B49502 standard; Protein; 265 AA.
XX
AC B49502;
XX
DT 09-MAR-2001 (first entry)
XX

XX DE Clone HYASC03.
 XX KW Human; 4 transmembrane superfamily receptor protein;
 KW endocrine; cardiovascular; cerebrovascular disease; neural disorder;
 KW reproductive; skin; renal system; autoimmune; hyperproliferative; ocular;
 KW bacterial infection; viral; fungal.
 XX OS Homo sapiens.
 XX PN WO200070076-A1.
 XX PD 23-NOV-2000.
 XX PF 18-MAY-2000; 2000WO-US13504.
 XX PR 19-MAY-1999; 99US-0135122.
 PR 03-JUN-1999; 99US-0137797.
 PR 11-JUN-1999; 99US-0138573.
 PR 18-AUG-1999; 99US-0149447.
 PR 28-JAN-2000; 2000US-0178770.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Ruben SM, Ni J, Fan P, Roschke V, Shi Y, Komatsoulis GA;
 PI Rosen CA;
 XX WPI; 2001-007502/01.
 DR N-PSDB; C90012.
 XX PT Isolated nucleic acid molecule encoding human soluble 4 transmembrane
 PT superfamily receptor protein, useful for diagnosing, treating and/or
 PT preventing disorders e.g. Alzheimer's, cancer and arrhythmia.
 XX PS Claim 11; Pages 278-279; 297pp; English.
 XX CC The present invention relates to isolated nucleic acids and proteins
 CC encoding human soluble 4 transmembrane superfamily receptor protein (see
 CC C90012-C90023 and B49502-B49513). The present sequence is one such
 CC protein. The present protein can be used to screen for binding partners
 CC and molecules which modify its activity. Antibodies specific for the
 CC present protein can be used to treat and/or prevent diseases associated
 CC with aberrant expression or activity of the present protein e.g.
 CC endocrine disorders e.g. Addison's disease, (cardio)vascular diseases
 CC e.g. arrhythmia and atherosclerosis, cerebrovascular diseases, neural
 CC disorders e.g. Alzheimer's and Parkinson's disease, reproductive
 CC disorders, skin disorders e.g. psoriasis, renal system disorders e.g.
 CC nephritis, (auto)immune system disorders e.g. graft vs. host disease,
 CC hyperproliferative disorders e.g. neoplasms of the pancreas, ocular
 CC disorders e.g. glaucoma and infections caused by bacteria, viruses and
 CC fungi.
 XX SQ Sequence 265 AA;
 Query Match 13.4%; Score 147.5; DB 22; Length 265;
 Best Local Similarity 29.2%; Pred. No. 1.1e-08;
 Matches 50; Conservative 32; Mismatches 66; Indels 23; Gaps 7;
 QY 2 AEPFVKVTRTSSPAQGAASVALRDLGVRSRLGALMLQLVLGLLVWALIADTPYH 61
 DB 5 AASPYPTEPVSQIRG---LAGLRCDDPYLRGALGRKVAQVILLALIAFICI-ETIMA 59
 QY 62 LYPAYG--WVWFVAVLMTIVFNLYLFOLHMKLYMPVPLVLMIFNISATVLYITAF 119
 DB 60 CSPCEGLYFFVSCSAFVGVLLIMFSLNLRIPQINWLTDLV-NTG-----LSAF 113
 QY 120 IACSAVDLTSLRGRTPNQRA-----AASFACLVMTAYGVSAFFSQAWR 166
 DB 114 IFFIASIVLAAL-----NHRAGAEIAAVIFGFLATAAYAVNTFLAVQKWR 158
 RESULT 9

XX DE P81879 standard; protein; 153 AA.
 XX AC P81879;
 XX DT 28-DEC-1990 (first entry)
 XX DE Sequence of full-length human T-cell protein derived from mature
 DE T cells.
 XX KW MAL protein; T-lymphocyte; leukaemia.
 XX OS Homo sapiens.
 XX PN WO8807549-A.
 XX PD 06-OCT-1988.
 XX PF 23-MAR-1988; 88WO-US00933.
 XX PR 26-MAR-1987; 87US-0031316.
 XX PA (UYIA-) YALE UNIV.
 XX PI Weissman SM, Alonso MA;
 XX WPI; 1988-292840/41.
 DR N-PSDB; n80218.
 XX PT Purified human T-cell protein and nucleotide sequence -
 PT used in the study of T-cell development and lymphocytic
 PT leukaemia(s)
 XX PS Claim 3; Pages 34-35; 51pp; English.
 XX CC Novel purified human T-cell protein is claimed. Four amphipathic domains
 CC defined by AAs 15-41, 53-75, 95-113 and 126-148. Flanking peptides are
 CC defined by AAs 1-14, 42-52, 76-94, 114-125 and 149-153. One or more of
 CC these relatively polar peptides may be used as peptide Ags. to produce
 CC antibodies specific against mature T-cells. Preferred antigen are those
 CC defined by AA segments 76-94 and 114-125. Also claimed is polynucleotide
 CC which encodes at least a portion of the T-cell protein. DNA composition
 CC may be used as a probe for detecting T-cells which are active in MAL
 CC protein prodn.
 XX SQ Sequence 153 AA;
 Query Match 13.1%; Score 144; DB 9; Length 153;
 Best Local Similarity 29.4%; Pred. No. 1.3e-08;
 Matches 42; Conservative 26; Mismatches 59; Indels 16; Gaps 5;
 QY 22 SVSALRPDLGVRSRLGALMLQLVLGLLVWALIADT--PYHLYPAYGWVNFVFLWLVLV 79
 DB 17 SVFTLTPDL-----LFFEFIFGGLVWLVLVASSLVPPWL--VGGWVIFSVFCFVA 65
 QY 80 TIVLFNLYLQLHMKLYMPVPLVLMIFNISATVLYITA-FIACSAVDLTSLRGRTPYN 138
 DB 66 TTTILILYIGAHGG--ETSWVTIDAAYHCTAALFYISASVLEALATIMTGDGFTYRHY 123
 QY 139 QRAAASFFACLVMTAYGVSAFFS 161
 DB 124 ENLAADVFSYIATILYVHVAFS 146
 RESULT 10
 P80929
 ID P80929 standard; protein; 153 AA.
 XX AC P80929;
 XX DT 28-DEC-1990 (first entry)

DE Sequence of human T-cell protein designated MAL.
 XX Lymphocytic leukaemia; antigen; diagnosis.
 KM Homo sapiens.
 XX MO807549-A.
 XX
 XX 06-OCT-1988.
 XX
 XX 23-MAR-1988; 88WO-US00933.
 XX
 XX 26-MAR-1987; 87US-0031316.
 XX
 XX (UYVA-) YALE-UNIT.
 XX Weissman SM, Alonso MA;
 XX
 XX WPI; 1988-292840/41.
 DR N-PSDB; N80218.
 XX
 XX Purified human T-cell protein and nucleotide sequence -
 PT used in the study of T-cell development and lymphocytic
 PT Leukemia(s)
 XX
 XX Claim 1; Pages 34-35; 51pp; English.
 XX
 XX MAL protein is produced in stages II and II/III, not stage I, T cells.
 CC It has four distinct amphipathic domains, each of which is flanked
 CC by a relatively polar peptide domain whose composition is predictive of
 CC a beta-pleat structure that would be stable in an aqueous environment.
 CC Flanking peptides defined by AAs 1-14, 42-52, 76-94, 76-94 and 114-125
 CC and are claimed.
 CC
 CC Sequence 153 AA:
 SQ
 Query Match 13.1%; Score 144; DB 9; Length 153;
 Best Local Similarity 29.4%; Pred. No. 1.3e-08;
 Matches 42; Conservative 26; Mismatches 59; Indels 16; Gaps 5;
 OY 22 SVSALRPDLGFVRSRLGALMLDLVLGALVWALITADT--PYHLPAVGWVWVAVFLMIV 79
 Db 17 svftltpdl-----lftelftfglywlvavslvppl--vggwvlvsvctva 65
 OY 80 TIVLFNLXYLQLMHKLYMWPVLMIFNLSATVLYTFA-FIACSAAVDLTSLRGTRPN 138
 Db 66 tcllllylllgahg--etawcldaeyhctaalfysasvlealeatlmtldgtfyrhph 123
 OY 139 QRAAAFACLVMIAYGVSAFFS 161
 Db 124 enlaavfysylacillyvhavfs 146
 DE
 XX
 XX Human ORFX ORF2711 polypeptide sequence SEQ ID NO:5422.
 XX
 XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KM vulnary; antiparasitic; antiparkinsonian; neurotropic; neuroprotective;
 KM anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KM immunostimulant; thrombolytic; coagulant; vasotrophic; antidiabetic;
 KM hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KM antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KM antinaeemic; gene therapy; cancer; proliferative disorder; hypertension;
 KM neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KM cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;

KM cholesterol ester storage; systemic lupus erythematosus; infection;
 KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KM bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KM thrombosis; contraceptive.
 XX
 XX Homo sapiens.
 XX
 XX MO200058473-A2.
 XX
 XX 05-OCT-2000.
 XX
 XX 31-MAR-2000; 2000MO-US08621.
 XX
 XX 31-MAR-1999; 99US-0127607.
 XX
 XX 02-APR-1999; 99US-0127636.
 XX
 XX 05-APR-1999; 99US-0127728.
 XX
 XX 30-MAR-2000; 2000US-0540763.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 XX Shinkets RA, Leach M;
 XX
 XX WPI; 2000-602362/57.
 DR N-PSDB; C77156.
 XX
 XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX
 XX Claim 11; Page 4607-4608; 5507pp; English.
 XX
 XX C74446 to C77606 encode the proteins given in B40237 to B43397, which
 CC represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antiparasitic; antiparkinsonian; neurotropic; neuroprotective; osteopathic;
 CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
 CC cardiant; thrombolytic; coagulant; vasotrophic; antidiabetic; hypotensive;
 CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
 CC antiviral; antifungal; antirheumatic; antithyroid; and antinaeemic. The
 CC sequences can be used for determining the presence of or predisposition
 CC to, or preventing or treating pathological conditions associated with an
 CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be
 CC used to treat cancers, proliferative disorders, neurodegenerative
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
 CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
 CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive.
 CC
 CC Sequence 276 AA:
 SQ

Query Match 12.5%; Score 137.5; DB 21; Length 276;
 Best Local Similarity 25.6%; Pred. No. 1.6e-07;
 Matches 45; Conservative 29; Mismatches 79; Indels 23; Gaps 4;
 OY 9 STRSSPAQAEASVSLRPDLGFVRSRLGALMLDLVLGALVWALITADT-PYHLPAVYGW 68
 Db 12 tttsssglsgpmulvgspra-----ltqplglltllqivscvafsfavagatgsmgw 67
 OY 69 VMFAAVLMLVTYLVFLVLYL-----FQLMHKLYMWPVLMIFNLSATVLYTFAFIC 122
 Db 68 smfwcfcfsvtlllllvelcogdarfpisvwnpftfacyaalfcsaillptlyv-- 125
 OY 123 SAAVDLTSLRGTRPNQRAAAFACLVMIAYGVSAFFSYOANRGVGSNATSQMA 178
 Db 126 -----qflahgsrdhaataatffsciacavayatev-----avtrrapslltgyma 170

CC downregulated in astrocytoma. Therefore restoring its expression
CC could be useful for the treatment of astrocytomas. Since it is
CC a multiple membrane spanning protein, gene therapy would be
CC necessary.

XX
SQ Sequence 322 AA;

Query Match 12.5%; Score 137.5; DB 21; Length 322;
Best Local Similarity 25.6%; Pred. No. 2e-07;
Matches 45; Conservative 29; Mismatches 79; Indels 23; Gaps 4;

QY 9 STPTSSPAQGAERASVALRDLGFVNSRLGALMLDLVLGLVALLADPPHYLPAYGW 68
D 12 ttttssglspsmlygspra---lcpqlgllrlqlvscvafslvasvgawtsgmgnw 67
QY 69 VMFVAVFLMVTIVLNLV-----FQLMKILYMPVLMIFNLSAVLYTATAC 122
D 68 smltwcstsvlllllvefcglqatrlpswrflptlctacyaalfclsaslllyptlyv-- 125
QY 123 SAAVDLTSLNGTRPYNOAAASFACILMIAYGVSAFFSYOAGVGNATASOMA 178
D 126 -----qflshgysrdhalaatlfcslacvayatev-----awtrarpgetlgyma 170

RESULT 14

ID Y99349 standard; Protein; 322 AA.

XX Y99349;

DT 08-AUG-2000 (first entry)

DE Human PRO1110 (UNQ53) amino acid sequence SEQ ID NO:31.

KW Human: PRO polypeptide; membrane bound protein; receptor; diagnosis;
transmembrane; secretion; immunoadhesion; pharmaceutical; screening.

XX Homo sapiens.

PN W0200012708-A2.

PD 09-MAR-2000.

XX 01-SEP-1999; 99WO-US20111.

XX 01-SEP-1998; 98US-0098716.

PR 01-SEP-1998; 98US-0098749.

PR 02-SEP-1998; 98US-0098803.

PR 02-SEP-1998; 98US-0098821.

PR 09-SEP-1998; 98US-0098843.

PR 09-SEP-1998; 98US-0098956.

PR 09-SEP-1998; 98US-0098958.

PR 09-SEP-1998; 98US-0098962.

PR 10-SEP-1998; 98US-0099642.

PR 10-SEP-1998; 98US-0099741.

PR 10-SEP-1998; 98US-0099754.

PR 10-SEP-1998; 98US-0099763.

PR 10-SEP-1998; 98US-0099792.

PR 10-SEP-1998; 98US-0098808.

PR 10-SEP-1998; 98US-0098812.

PR 10-SEP-1998; 98US-0098815.

PR 15-SEP-1998; 98US-0100385.

PR 15-SEP-1998; 98US-0100388.

PR 15-SEP-1998; 98US-0100390.

PR 16-SEP-1998; 98US-0100584.

PR 16-SEP-1998; 98US-0100627.

PR 16-SEP-1998; 98US-0100661.

PR 16-SEP-1998; 98US-0100662.

PR 16-SEP-1998; 98US-0100664.

PR 17-SEP-1998; 98US-0100683.
PR 17-SEP-1998; 98US-0100684.
PR 17-SEP-1998; 98US-0100710.
PR 17-SEP-1998; 98US-0100711.
PR 17-SEP-1998; 98US-0100919.
PR 17-SEP-1998; 98US-0100930.
PR 18-SEP-1998; 98US-0100848.
PR 18-SEP-1998; 98US-0100849.
PR 18-SEP-1998; 98US-0101014.
PR 18-SEP-1998; 98US-0101068.
PR 18-SEP-1998; 98US-0101071.
PR 22-SEP-1998; 98US-0101279.
PR 23-SEP-1998; 98US-0101471.
PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101475.
PR 23-SEP-1998; 98US-0101476.
PR 23-SEP-1998; 98US-0101477.
PR 23-SEP-1998; 98US-0101479.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102240.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102330.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102687.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103449.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103395.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103678.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104987.
PR 20-OCT-1998; 98US-0105000.
PR 20-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105104.
PR 22-OCT-1998; 98US-0105169.
PR 22-OCT-1998; 98US-0105266.
PR 26-OCT-1998; 98US-0105593.
PR 26-OCT-1998; 98US-0105694.
PR 27-OCT-1998; 98US-0105807.
PR 27-OCT-1998; 98US-0105881.
PR 27-OCT-1998; 98US-0105882.
PR 27-OCT-1998; 98US-0106062.
PR 28-OCT-1998; 98US-0106023.
PR 28-OCT-1998; 98US-0106029.
PR 28-OCT-1998; 98US-0106030.
PR 28-OCT-1998; 98US-0106032.
PR 28-OCT-1998; 98US-0106033.
PR 28-OCT-1998; 98US-0106178.
PR 29-OCT-1998; 98US-0106248.
PR 29-OCT-1998; 98US-0106384.
PR 29-OCT-1998; 98US-0106500.
PR 30-OCT-1998; 98US-0106464.
PR 03-NOV-1998; 98US-0106856.
PR 03-NOV-1998; 98US-0106902.

PR 03-NOV-1998; 98US-0106905.
 PR 03-NOV-1998; 98US-0106919.
 PR 03-NOV-1998; 98US-0106932.
 PR 03-NOV-1998; 98US-0106934.
 PR 10-NOV-1998; 98US-0107783.
 PR 17-NOV-1998; 98US-0108775.
 PR 17-NOV-1998; 98US-0108779.
 PR 17-NOV-1998; 98US-0108787.
 PR 17-NOV-1998; 98US-0108788.
 PR 17-NOV-1998; 98US-0108801.
 PR 17-NOV-1998; 98US-0108802.
 PR 17-NOV-1998; 98US-0108806.
 PR 17-NOV-1998; 98US-0108807.
 PR 17-NOV-1998; 98US-0108867.
 PR 17-NOV-1998; 98US-0108925.
 PR 18-NOV-1998; 98US-0108848.
 PR 18-NOV-1998; 98US-0108849.
 PR 18-NOV-1998; 98US-0108850.
 PR 18-NOV-1998; 98US-0108851.
 PR 18-NOV-1998; 98US-0108852.
 PR 18-NOV-1998; 98US-0108856.
 PR 18-NOV-1998; 98US-0108904.
 PR 18-NOV-1998; 98US-0108904.

(GETH) GENENTECH INC.

PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
 DR WPI: 2000-237871/20.
 DR N-PSDB; A37031.

XX New mammalian DNA sequences encoding transmembrane, receptor or
 PT secreted PRO polypeptides, useful for screening of potential peptide or
 PT small molecule inhibitors of the relevant receptor/ligand interactions

XX Claim 12; Fig 20; 773pp; English.

CC A37022 to A37144 encode the new isolated human transmembrane, receptor
 CC or secreted PRO polypeptides given in 199340 to 199462. The
 CC transmembrane and receptor PRO proteins can be used for screening of
 CC potential peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences
 CC encoding them have various industrial applications, including uses as
 CC pharmaceutical and diagnostic agents. A37145 to A37330 represent
 CC PCR primers and hybridization probes used in the isolation of the PRO
 CC polypeptides from the present invention.

XX Sequence 322 AA;

Query Match 12.5%; Score 137.5; DB 21; Length 322;
 Best Local Similarity 25.6%; Pred. No. 2e-07;

Matches 45; Conservative 29; Mismatches 79; Indels 23; Gaps 4;

QY 9 SRTSSPAAGASVSALRPDLGFRSRIGALMLQVLGLLWALLIDTPYHLYPAWG 68
 DB 12 ttttssggsgsmlygsppa-----ltqplgllrlqlvstcaistlsvsawtgsimgw 67
 QY 69 VAEVAVFLMTLVITIVFENLYL-----FQLHMKLYVMPMPVLYLMFNISATVLYTAFIAC 122
 DB 68 smftwcfctsvcllllvelcglgarflswrnfplftacynaalcasaslyptty-- 125
 QY 123 SAAYDLTISRGRPIYNGRAASFFACLYMAYAGVSAFSTYQAMKGVGSNAATSOA 178
 DB 126 -----qfshgrdrdhalaatfisciacvayatev-----awtrarpgeitgyma 170

RESULT 15

ID B56922 standard; Protein; 144 AA.

AC B56922;

DT 13-MAR-2001 (first entry)

XX Human prostate cancer antigen protein sequence SEQ ID NO:1500.

DE Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 XX neuroprotective; cytosolic; cardioprotective; immunomodulatory; muscular;
 KW vulnere; gastrointestinal; nephrotoxic; antiinfective; gynaecological;
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 KW wound; infectious disease.

XX Homo sapiens.

OS WO200055174-A1.

PN 21-SEP-2000.

PD 08-MAR-2000; 2000WO-US05988.

PF 12-MAR-1999; 99US-0124270.

PR (HUMA-) HUMAN GENOME SCI INC.

PA (ROSE/) ROSEN C A.

PI Rosen CA, Ruben SM;

XX WPI: 2000-587513/55.

DR N-PSDB; F16125.

XX Prostate cancer associated gene sequences, referred to as prostate
 PT cancer antigens, useful for treatment, prevention, and diagnosis of
 PT disorders such as prostate cancer

PS Claim 11; Page 1939-1940; 2338pp; English.

XX F15566 to F16505 encode the human prostate cancer associated proteins.
 CC called prostate cancer antigens, given in B56363 to B57302. The prostate
 CC cancer antigens can have neuroprotective, cytosolic, cardioprotective,
 CC immunomodulatory, muscular, vulnere, gastrointestinal, nephrotoxic,
 CC antiinfective, gynaecological and antibacterial activities, and can be
 CC used in gene therapy. The prostate cancer antigen polynucleotides may be
 CC used for detection of prostate cancer, chromosome identification, as
 CC chromosome markers, and for numerous other diagnostic or research
 CC purposes. The prostate cancer antigens may be used to treat disorders
 CC such as neural, immune, muscular, reproductive, gastrointestinal,
 CC pulmonary, cardiovascular, renal, and proliferative disorders, wounds,
 CC and infectious diseases. F15506 to F16514 to B57303 represent sequences
 CC used in the exemplification of the present invention.

XX Sequence 144 AA;

Query Match 12.4%; Score 137; DB 21; Length 144;
 Best Local Similarity 28.0%; Pred. No. 7.7e-08;

Matches 37; Conservative 24; Mismatches 59; Indels 12; Gaps 3;

QY 46 VLGLLWALLIDTPYHLYPAWGMEVAVETMLVTIVFENLYLFOHMKLYVMPVLYM 105
 DB 13 lfglwllvassvnpipldlgwvmfvstafiffellflgmsgmvgq-danvfidf 71
 QY 106 IFNISATVLYTAFIACSAAYDL-----TSIRG-----TPRYNGRAASFFACLYMAY 154
 DB 72 aynhtvtyfygatlileaaatslndhntcttgpllsdqynlnuvasstfatmtacy 131
 QY 155 GVSAAFFSYOAMR 166
 DB 132 gcslglahttrvr 143

Search completed: May 2, 2001, 15:10:43
 Job time: 48 sec

C:Genetics:
 A:Gene: CESP.F28H1.4
 A:Map position: 1
 A:Introns: 4/1; 66/3; 108/3; 150/1; 188/3; 235/3

Query Match 14.4%; Score 158; DB 2; Length 281;
 Best Local Similarity 28.6%; Pred. No. 2.1e-06;
 Matches 50; Conservative 27; Mismatches 76; Indels 22; Gaps 5;

QY 18 GABASVALRPDGFVRSRLGALMLQVLVGLVMAIADTPYHILPAWGVAFLM 77
 DB 104 GPAVRLEFFHDEYIRITLGGIKIVICLLITFFVMMGRAY-YTGVMATFVSSVCI 162
 QY 78 LVTVLEFNLVLEFQIHKMLVMPVPLV-----MIFNISATVLYTTAFIACSAV 126
 DB 163 FVTTSLTLEFVVDLPSINIVICLSTRTEIIIEQVNYCAWVFEFLA--ACVLAV 220
 QY 127 DLISLNGTRRYNORRAASFPACLVMAVGSAPFSQANRG-----VGSNATSQ 176
 DB 221 ASSQFNGTFAM--ALAAFFAGMCAVGPDCYLKFLSMKNMERATGSGNPVYIQ 272

RESULT 3

T-cell surface glycoprotein MAL, splice form a - human
 A:Accession: A29472

N:Alternate names: MAL, proteolipid

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 20-Jun-2000

A:Accession: A29472; S40076; S40077; S40078; A54680; I38009; S36933; S38934; S38

R:Alonso, M.A.; Weissman, S.M. 84, 1997-2001, 1987

A:Title: CDNA cloning and sequence of MAL, a hydrophobic protein associated with human T

A:Reference number: A29472; MUID:87175600

A:Accession: A29472

A:Molecule type: DNA

A:Residues: 1-153 <LMO>

A:Cross-references: GB:M15800; NID:9187297; PIDN:AAA6196.1; PID:9307157

R:Rancano, C.; Rubio, T.; Alonso, M.A.
 submitted to the EMBL Data Library, December 1993

A:Description: Alternative splicing of human T-cell specific MAL mRNA and its correlatio

A:Reference number: S40076

A:Accession: S40076

A:Molecule type: mRNA

A:Residues: 1-153 <RAN>

A:Cross-references: EMBL:X76678; NID:9435477; PIDN:CAA54100.1; PID:9435478

A:Note: MAL-a

A:Accession: S40077

A:Molecule type: mRNA

A:Residues: 1-87,130-153 <RAN>

A:Cross-references: EMBL:X76679; NID:9435479; PIDN:CAA54101.1; PID:9435480

A:Note: MAL-b

A:Accession: S40079

A:Molecule type: mRNA

A:Residues: 1-31,130-153 <RAP>

A:Cross-references: EMBL:X76681; NID:9435481; PIDN:CAA54103.1; PID:9435482

A:Note: MAL-d

A:Accession: S40078

A:Molecule type: mRNA

A:Residues: 1-31,88-153 <RAA>

A:Cross-references: EMBL:X76680; NID:9435483; PIDN:CAA54102.1; PID:9435484

A:Note: MAL-c

R:Rancano, C.; Rubio, T.; Alonso, M.A.

Genomics 21, 447-450, 1994

A:Title: Alternative splicing of human T-cell-specific MAL mRNA and its correlation with

A:Reference number: A54680; MUID:94375076

A:Accession: A54680

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-153 <RA2>

A:Cross-references: GB:X76678; NID:9435477; PIDN:CAA54100.1; PID:9435478

R:Rancano, C.; Rubio, T.; Correas, I.; Alonso, M.A.
 J. Biol. Chem. 269, 8159-8164, 1994

A:Title: Genomic structure and subcellular localization of MAL, a human T-cell-specific

A:Reference number: I38009; MUID:94179190

A:Accession: I38009

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-31 <RES>

A:Cross-references: EMBL:X76220; NID:9433225; PID:91200084

A:Experimental source: placenta

A:Note: Submitted to the EMBL Data Library, November 1993

C:Genetics:

A:Gene: GDB:MAL

A:Cross-references: GDB:119374; OMIM:188860

A:Map position: 2cen-2q13

A:Introns: 31/3; 87/3; 129/3

C:Superfamily: T-cell surface glycoprotein MAL

C:Keywords: alternative splicing; endoplasmic reticulum; glycoprotein; T-cell; trans

F.1-153/Product: T-cell surface glycoprotein MAL, splice form a #status predicted <MA

F.1-87,130-153/Product: T-cell surface glycoprotein MAL, splice form b #status predic

F.1-31,88-153/Product: T-cell surface glycoprotein MAL, splice form c #status predic

F.1-31,130-153/Product: T-cell surface glycoprotein MAL, splice form d #status predic

Query Match 13.9%; Score 153; DB 2; Length 153;

Best Local Similarity 30.2%; Pred. No. 3.3e-06;

Matches 45; Conservative 25; Mismatches 61; Indels 18; Gaps 6;

QY 22 SVSALRPDGFVRSRLGALMLQVLVGLVMAIADTPYHILPAWGVAFLM 79
 DB 17 SVFTLPD-----LFEFFFGVILVSLVMPV--VQGVMPFVSCFVA 65
 QY 80 TVLEFNLVLEFQIHKMLVMPVPLV-----MIFNISATVLYTTAFIACSAV 137
 DB 66 TTTLLIILYIGAHG--EISWVTLDAHYCTALPILASV--LEALATITMDDGFYRNY 122
 QY 138 NORAAAFACLVMAVGSAPFSQANRG-----VGSNATSQ 176
 DB 123 HENIAAVFSYATILLYVHAVFSLIRMK 151

RESULT 4

hypothetical protein - human (fragment)
 A:Accession: I38891

C:Species: Homo sapiens (man)

C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 29-Sep-1999

A:Accession: I38891

R:Laubner-Rieske, A.; Thiebe, R.; Zachau, H.G.

Gene 159, 199-202, 1995

A:Title: Searching for non-V kappa transcripts from the human immunoglobulin kappa 10

A:Reference number: I38891; MUID:95347597

A:Accession: I38891

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-148 <RES>

A:Cross-references: EMBL:U17077; NID:91000711; PIDN:AAA6738.1; PID:91000712

C:Genetics:

A:Gene: BENE

C:Superfamily: T-cell surface glycoprotein MAL

Query Match 13.5%; Score 148.5; DB 2; Length 148;

Best Local Similarity 30.2%; Pred. No. 7.6e-06;

Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;

QY 39 ALMLQVLVGLVMAIADTPYHILPAWGVAFLM 97
 DB 24 AFPELIGFLVIMVAT-HIYPLDGLVWVYSLTSLISIMPLSLFGEFYKR--F 80
 QY 98 VMPVLMIFNISATVLYTT-AFIACSAVDTLSGTRPYNORAAAFACLVMAV 156
 DB 81 ESMRVLDLSYHGTGLYSAAVLQVHATVSEKLDPRIVYINSAAFFAFATLTYL 140
 QY 157 SAFFSY 162

DB 141 HAFSIV 146

RESULT 5

S68406

vesicular integral membrane protein VIP17 - dog

N:Alternate names: proteolipid VIP17; T-cell-specific MAL protein homolog VIP17

C:Species: Canis lupus familiaris (dog)

C>Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 29-Sep-1999

C:Accession: S68406; S68399

R:Zachetti, D.; Peranen, J.; Murata, M.; Fiedler, K.; Simons, K.

FEBS Lett. 377, 465-469, 1995

A:Title: VIP17/MAL, a proteolipid in apical transport vesicles.

A:Reference number: S68399; MUID:96140569

A:Accession: S68406

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-153 <ZAC>

A:Cross-references: EMBL:X92505; NID:g1054712; PID:CA63261.1; PID:g1054713

A:Accession: S68399

A:Molecule type: protein

A:Residues: 3-16;120-131 <ZAM>

A:Experimental source: kidney; cell-line Madin-Darby canine kidney cell

C:Function:

A:Pathway: myelin biogenesis

C:Superfamily: T-cell surface glycoprotein MAL

Query Match

Best Local Similarity 27.5%; Score 145.5; DB 2; Length 153;

Matches 46; Conservative 25; Mismatches 73; Indels 23; Gaps 4;

DB 3 PAAASGSSSLP---SGFSVFTEPDL-----LFEFEFIRGILWMIASLVPIL 50

QY 5 PKVSTRTSSPAOGAASVSALRPDLGFVRSRLGALMLQLVGLLWALADTPHYLYP 64

DB 65 AIGWVFAVFLMVLIVTIVFNLYLLEQLH-----MKIYMPWPLVLMIFNLSAVLYITAP 119

DB 51 VOGWVFAVFLMVLIVTIVFNLYLLEQLH-----MKIYMPWPLVLMIFNLSAVLYITAP 110

QY 120 IACSAVDLSLRGFRPYNORRAASFEACLVMIAGVSAPFSYQAWR 166

DB 111 IGMQESYTY-----KQYHENSIAVVFSTYVATLLVYHAFSLIRMK 151

RESULT 6

T29152

hypothetical protein F47B3.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T29152

R:Du, Z.; Le, T.T.

submitted to the EMBL Data Library, April 1997

A:Description: The sequence of C. elegans cosmid F47B3.

A:Reference number: 220579

A:Accession: T29152

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-156 <DUZ>

A:Cross-references: EMBL:U97017; PIDN:AAB52358.1; GSPDB:GN00019; CESP:F47B3.3

A:Experimental source: strain Bristol N2; clone F47B3

C:Genetics:

A:Gene: CESP:F47B3.3

A:Map position: 1

A:introns: 25/1; 63/3; 110/3

Query Match

Best Local Similarity 29.4%; Score 141; DB 2; Length 156;

Matches 45; Conservative 23; Mismatches 63; Indels 22; Gaps 5;

QY 40 LMLDGLVGLLWALADTPHYLYPFAVFLMVLIVTIVFNLYLLEQLHMKLYMP 99

DB 111 IGMQESYTY-----KQYHENSIAVVFSTYVATLLVYHAFSLIRMK 151

DB 1 MKIVCIIVLCILFIFVMMGPAY-YTGVNATFVSSVIGIFVTSLLTLFLRVVDLPISIN 59

QY 100 WPLVY-----MINISATVLYITAFICSAVDLTSRGFRPNORRAASFFAC 148

DB 60 WIVCISTREIILIFQEMVYCFAMTVFFFLA--ACVLAVASQFRGFAM--AIAFFAF 114

QY 149 LVMIAGVSAPFSYQAWR-----VGSNATSQ 176

DB 115 GACVAGFDCYIKELSLWKNNRATGGSNPVITQ 147

RESULT 7

T19664

hypothetical protein C33A12.9b - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T19664

R:Wilkinson, J.

submitted to the EMBL Data Library, January 1996

A:Reference number: Z19159

A:Accession: T19664

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-242 <WIL>

A:Cross-references: EMBL:268493; PIDN:CAA92794.1; GSPDB:GN00022; CESP:C33A12.9b

A:Experimental source: clone C33A12

C:Genetics:

A:Gene: CESP:C33A12.9b

A:Map position: 4

A:introns: 60/3; 113/3; 181/3

C:Superfamily: Caenorhabditis elegans hypothetical protein C33A12.9b

Query Match

Best Local Similarity 20.9%; Score 95.5; DB 2; Length 242;

Matches 32; Conservative 25; Mismatches 43; Indels 53; Gaps 5;

QY 42 LQIVGLLWALADTPHYLYPAG-----WVWFV-----A 73

DB 65 LIRVIVPLILFYPICFT-FYLIPALGVCRRPEYFGAWIYITNSAGLRNSFNLYS 123

QY 74 VFLMVLIVFNLYL-----QLMKLYMPWPLVLMIFNLSATVLYITAFICSAVDLT 129

DB 124 IIFWLVASVIVNLFELVKKYRQAKTOLVOIPQSKAEFSITVTLVVIIFILNGC---- 179

QY 130 SLRGFRPYNORRAASFEACLVMIAGVSAPFSY 162

DB 180 -----FVLYMFESYGSYSPTSY 196

RESULT 8

I39294

McLeod syndrome-associated protein XK - human

N:Alternate names: probable membrane transport protein

C:Species: Homo sapiens (man)

C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 01-Dec-2000

C:Accession: I39294; S69126

R:Ho, M.; Chelly, J.; Carter, N.; Dane, A.; Crocker, P.; Monaco, A.P.

Cell 77, 869-880, 1994

A:Title: Isolation of the gene for McLeod syndrome that encodes a novel membrane trar

A:Reference number: A54300; MUID:94273191

A:Accession: I39294

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-444 <REMS>

A:Cross-references: EMBL:232684; NID:g515872; PID:g515873

R:Khamlich, S.; Bailey, P.; Blanchard, D.; Goossens, D.; Cartton, J.P.; Bertrand, O.

Eur. J. Biochem. 228, 931-934, 1995

A:Title: Purification and partial characterization of the erythrocyte Kx protein defi

A:Reference number: S69126; MUID:95255304

A:Accession: S69126

A:Status: preliminary

A:Molecule type: protein

A:Residues: 7-22 <KHA>
 C:Genetics:
 A:Gene: GDB:XK
 A:Cross-references: GDB:120459; OMIM:314850
 A:Map position: Xp21.2-Xp21.1
 C:Keywords: phosphoprotein; transmembrane protein

Query Match 8.7%; Score 95.5; DB 2; Length 444;
 Best Local Similarity 22.4%; Pred. No. 0.65;
 Matches 39; Conservative 28; Mismatches 66; Indels 41; Gaps 8;

QY 13 SSPAGAEASVSALRPDLGFVRSRGLMLQLVGLVWALIA-DPPIHLYPA-YGVWM 70
 DB 148 SAPQLQLQIYISMODVVGSLMTISLSIVIGALRCNLIKIKIDEYKVNRLA 207
 QY 71 FPAVFLW-----LVTVLENLVLPOLHMKLYMPPLVLMIFNISATVLYTAFLAC 122
 DB 208 YVCIFLMRSFEIATRVVLYVLTSLV-----KTVWVVILLINFSFELYPILFMC 258
 QY 123 SAADVLTSLRGTRPYNQ-----RAASFACLYMIAY-GVSASFSTQAMRGV 168
 DB 259 SCS-----PPENIEKALSRVGTITVLCFLLTYTGIMF-----CWGAV 298

RESULT 9

S13585
 most protein precursor - Pseudomonas stutzeri
 C:Species: Pseudomonas stutzeri
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 08-Oct-1999
 C:Accession: S13585
 R:Zunft, W.G.; Viebrock-Sambale, A.; Braun, C.
 Eur. J. Biochem. 192, 591-599, 1990
 A:Title: Nitrous oxide reductase from denitrifying Pseudomonas stutzeri. Genes for copper
 oxiase.
 A:Reference number: S13582; MUID:91006150
 A:Accession: S13585
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-276 <ZOU>
 A:Cross-references: EMBL:X53676; NID:945844; PIDN:CAA37717.1; PID:945850

Query Match 8.6%; Score 95; DB 2; Length 276;
 Best Local Similarity 24.3%; Pred. No. 0.46;
 Matches 43; Conservative 31; Mismatches 55; Indels 48; Gaps 9;

QY 23 VSALRPDLGFVRSRGLMLQLV-LGLVWA-----LIADRPYHLXPAYGMWF----- 71
 DB 111 IIALAVLVIGFCAALALVILVGVGLVGLMFLMFGFMIST-----LLGVFLAFAYVL 164
 QY 72 -----VAVFLMLVTVLEFNLVLEFOL-----HMKLYMPPLVLMIFNISATV 113
 DB 165 SGRVNEKSAAGLGVWFLVFLVDVLLVLLVLSSEKFPPELLPWILL-----NPTD 219
 QY 114 LY-----ITAFICSAADVLTSLRGTRPYNQRAASFACLYMIAYGVSASFSTQAMR 166
 DB 220 IYRLINSGFEGSGSAMGVLSGADLPV---PAAVLMICL-LAMIGVSLLAIAIFR 272

RESULT 10

YOECD
 sodium-glutamate symport carrier protein - Escherichia coli
 N:Alternate names: glutamate permease
 C:Species: Escherichia coli
 C:Date: 30-Jun-1991 #sequence_revision 31-Oct-1997 #text_change 16-Jun-2000
 C:Accession: G65166; A36524; S14031; J00489
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co-
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617
 A:Accession: G65166

A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA

A:Residues: 1-401 <BLAT>
 A:Cross-references: GB:A000442; GB:000096; NID:92367253; PIDN:AACT6677.1; PID:917900
 A:Experimental source: strain K-12, substrain MG1655
 R:Deutch, Y.; Yamato, I.; Anraku, Y.
 J. Biol. Chem. 265, 21704-21708, 1990
 A:Title: Nucleotide sequence of gits, the Na(+)/glutamate symport carrier gene of Esc
 A:Reference number: A36524; MUID:91072371

A:Accession: A36524

A:Molecule type: DNA

A:Residues: 1-377, 'S', 379-401 <DEG>

A:Cross-references: GB:D00626; NID:9216540; PIDN:BAA00517.1; PID:9216541

A:Experimental source: strain 829-78

R:Kaltman, M.; Gentry, D.R.; Cashel, M.

Mol. Gen. Genet. 225, 379-386, 1991

A:Title: Characterization of the Escherichia coli K12 gits glutamate permease gene.

A:Reference number: S14031; MUID:91203811

A:Accession: S14031

A:Molecule type: DNA

A:Residues: 1-401 <KAL>

A:Cross-references: EMBL:X17499; NID:941592; PIDN:CAA35540.1; PID:941593

C:Genetics:

A:Gene: gits

A:Map position: 82 min

C:Superfamily: sodium-glutamate symport carrier protein

C:Keywords: glutamate transport; transmembrane protein

Query Match 8.6%; Score 95; DB 1; Length 401;
 Best Local Similarity 22.6%; Pred. No. 0.65;
 Matches 47; Conservative 35; Mismatches 96; Indels 30; Gaps 6;

QY 1 MAEPKSVSTSTSSPAQAEASVSALRPDLGFVRSRLG-----ALMLQLVGLVWALI 55
 DB 179 VARLVKSTSTPNGLPDDQEVPTAFERKPDVGKMTSLVLIETIALICLTVGKIVALL 238
 QY 56 ADTPYHLXPAYGMWFVAVFLMVTIVFNLVLPOLHMKLYMPPLVLMIFNISATVLY 115
 DB 239 AGTAFEL-PTFVCVLFVGVILISGLSI-----NGFYRFFERAVSVLGNVLSLFL 287
 QY 116 ITAFICSAADVLTSLRGTRPYNQRAASFACLYMIAYGVSASFSTQAMRGVSNATS 175
 DB 288 AMALMGK-LWEIASL-----ALPMLALIVVQITFMALIAIFVTRMAGNNTDAA 336
 QY 176 QMAGYATTCATAPSGAEAAAGSQRVT 203
 DB 337 VLAAGH---CGFGIGATPTFATANNQAIT 361

RESULT 11

S32567
 A4 protein - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
 C:Accession: S32567
 R:Oliva, M.M.; Wu, T.C.; Yang, V.W.
 Arch. Biochem. Biophys. 302, 183-192, 1993
 A:Title: Isolation and characterization of a differentiation-dependent gene in the hu
 A:Reference number: S32567; MUID:93228341
 A:Accession: S32567
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-152 <OLI>
 A:Cross-references: EMBL:L09604; NID:9177899; PIDN:AAA35499.1; PID:9177900
 A:Gene: GDB:A4
 A:Cross-references: GDB:683190

Query Match 8.6%; Score 94.5; DB 2; Length 152;
 Best Local Similarity 21.3%; Pred. No. 0.3;
 Matches 38; Conservative 32; Mismatches 71; Indels 37; Gaps 7;

```

Query March 1998; Score 93; DB 2; Length 471;
Best Local Similarity 19.4%, Pred. No. 1.1;
Matches 42; Conservative 37; Mismatches 74; Indels 64; Gaps 9;

QY      39 ALMLQLVLGLL-----VMAL-----IADPYHLXPY----- 65
           ||| :||| :| | :| |
DB      165 AAMPLFLMGHLSHDREKERTVFFLLGTAYCAISIGLGIVGSPNLLIAAKLNIDF 224
           ||| :||| :| | :| |
QY      66 YGVV-MEPAVLELMVTITYLENLILE-----QLMKLYMPWPL----VLMINISATV 113
           ||| :||| :| | :| |
DB      225 VGMWMLGIIPMMLILIPMLTSLYLTKPNLENERKIKESIPWTLHRVIALIIIFATAAA 284
           ||| :||| :| | :| |
QY      114 LYTFAFICSAAVDFTSLRGTRPYNQRBAASFACLVMAIASVFASFFEQMRGGSN-- 171
           ||| :||| :| | :| |
DB      285 WFSKKITATGIS-----NPDTVIALLSAAVAVVVGVA-----QKEVARNTD 328
           ||| :||| :| | :| |
QY      172 -AATSOMAGYATTCATAPSGAEAAAGSQSRVTLQAS 207
           ||| :||| :| | :| |
DB      329 MGVLMLFGGGISLTSLTKTSAGSEALGGQVAATFSCA 365
           ||| :||| :| | :| |

RESULT 13
T32917
hypothetical protein K02F2.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
C:Accession: T32917
A:Maggil, L.; Goela, D.
Submitted to the EMBL Data Library, January 1998
A:Description: The sequence of C. elegans cosmid K02F2.
A:Reference number: Z21246
A:Accession: T32917
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-610 <MAG>
A:Cross-references: EMBL:AF043699; PTDN:AAB97568.1; GSPDB:GN000019; CESP:K02F2.6
A:Experimental source: Strain Bristol N2; clone K02F2

```

```

Query March 8.48; Score 92; DB 2; Length 471;
Best Local Similarity 19.48; Pred. No. 1.3;
Matches 42; Conservative 37; Mismatches 74; Indels 64; Gaps 9;

QY 39 ALMLQLVLGLL-----VVAL-----IADTPYLRYA----- 65
| | | | | | | | | | | | | | | | | | | | | |
Db 165 AAMPLAMGMLSHLDKEKHKTYVFLLLGLIAYCASIGGLGVGSPPLIAAKALNDF 224
| | | | | | | | | | | | | | | | | | | | | |
QY 66 YGVV-MEFAVFLPLMTIYVFNLYLF-----QLHKKLYMWPL-----VLMFNLSAVY 113
| | | | | | | | | | | | | | | | | | | | | |
Db 225 VGMMLGLSPMMLLPLMLLSYVILKPLNLNERVEKASIEPWLTHRVIALILFLATAAA 284
| | | | | | | | | | | | | | | | | | | | | |
QY 114 LYTLAFIACSAAYDFTLSGTRPYNORAAASPEACILMIYGSAAFFYSOANRGVSN-- 171
| | | | | | | | | | | | | | | | | | | | | |
Db 285 WIFSSKITAFGIS-----NPDYIALSAANVAVVEGVA-----QKREYARNND 328
| | | | | | | | | | | | | | | | | | | | | |
QY 172 -AATSOAGGYATTCAATPGAGAAAGSOSRYTLQAS 207
| | | | | | | | | | | | | | | | | | | | | |
Db 329 MGVLMLEFGGIGISLTILKRTSGASEALIGQVAAFTFSGA 365
| | | | | | | | | | | | | | | | | | | | | |

```


RESULT 15

T23328

hypothetical protein K04G2.9 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T23328

R:Gardner, A. submitted to the EMBL Data Library, July 1996

A:Reference number: 219727

A:Accession: T23328

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-208 <M1>

A:Cross-references: EMBL:Z75712; PIDN:CAB00046.1; GSPDB:GN00019; CESP:K04G2.9

A:Experimental source: clone K04G2

C:Genetics:

A:Gene: CESP:K04G2.9

A:Map position: 1

A:introns: 22/2; 57/3; 175/3

Query Match

Best Local Similarity 8.3%; Score 91; DB 2; Length 208;

Matches 45; Conservative 30; Mismatches 76; Indels 32; Gaps 8;

```

QY 8 VSTRSSPAOGAEASVSL---RPDLGFVRSRLGALMLQLVLLVWALADPPYHLP 64
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 17 VTTTREKTKREKHSWSCGHGPTDKNYCIGPLRIAEIPLCVIVCLITSV-FGPGP 75
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 65 AYGWVF-----VAVFMTVTIVLENLYLQLMK-LYMPVPLVMIFNISATVLYI 116
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 76 FRG-LIEGQTILLTVASVAMLTFFFLAYFFTLHLSHDFECWREADLLENVICAVLEI 134
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 117 TAFIA-----CSAVIDLS---LRGTRPYNOBAASPFACIWMYGVSAF 160
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 135 VLSIVAEAYTSGSWSNCH---DIGSDGIINHGCRITTEMAPASFLTIGIFALTAPL 191
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 161 STQ 163
   | | |
DB 192 THK 194

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Search completed: May 2, 2001, 15:11:00
 Job time: 65 sec

GenCore version 4.5
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OM protein - protein search, using sw model

May 2, 2001, 15:10:20 / Search time 9.56 Seconds

(Without alignments) 773.973 Million cell updates/sec

Title: US-09-602-597-4
Perfect score: 1101
Sequence: 1 MAEPFSKYSTRSSPAQGAEE.....GSOSRTVLQASMGALRGVSP 216

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	930	84.5	182	1	PLP_HUMAN
2	848	77.0	182	1	PLP_RAT
3	155	14.1	153	1	MAL_MOUSE
4	153	13.9	153	1	MAL_HUMAN
5	152	13.8	153	1	MAL_RAT
6	148.5	13.5	148	1	BENE_HUMAN
7	145.5	13.2	153	1	MAL_CANFA
8	131	11.9	296	1	MYDM_MOUSE
9	95	8.6	276	1	NOSY_PSEST
10	95	8.6	401	1	GUTS_ECOLI
11	94.5	8.6	152	1	AAP_HUMAN
12	93.5	8.5	446	1	SMVA_SALTY
13	92	8.4	496	1	IMPL_EBYC
14	90.5	8.2	404	1	B3AR_RAT
15	86.5	7.9	400	1	B3AR_CAVPO
16	86	7.8	351	1	B3AR_CAVPI
17	84	7.6	157	1	Y630_METJA
18	84	7.6	297	1	ENTL_HUMAN
19	82	7.4	455	1	B3AR_MOUSE
20	81.5	7.4	400	1	YEPO_YEAST
21	81	7.4	528	1	YEPO_YEAST
22	80.5	7.3	428	1	GPRX_ORYLA
23	80	7.3	305	1	CC91_YEAST
24	80	7.3	394	1	CC91_YEAST
25	79.5	7.2	405	1	B3AR_CANFA
26	79.5	7.2	476	1	GREL_BALAM
27	79.5	7.2	555	1	CSTRA_AQUAE
28	79	7.2	405	1	B3AR_CAVPI
29	78	7.1	678	1	YF48_MYCNU
30	77.5	7.0	379	1	CYB_SORCI
31	77.5	7.0	379	1	CYB_SORCI
32	77	7.0	312	1	ORF4_RAT
33	77	7.0	318	1	YBHN_ECOLI

34	77	7.0	412	1	Y663_METH	026759 methanobact
35	77	7.0	428	1	BCH2_RHOCA	P26171 rhodobacter
36	77	7.0	468	1	B1AR_PIG	028998 sus scrofa
37	77	7.0	525	1	DIE2_YEAST	P50706 saccharomyc
38	76.5	6.9	152	1	TOX4_BORPE	P04960 bordecella
39	76.5	6.9	318	1	NDIM_TRIVU	078707 trichosurus
40	76.5	6.9	355	1	OPSB_ASTFA	P51472 astyanax fa
41	76.5	6.9	395	1	Y306_MYCPN	P75343 mycoplasma
42	76.5	6.9	401	1	YEDE_SALTY	006400 salmonella
43	76.5	6.9	546	1	LNT_TREPA	083279 treponema p.
44	76	6.9	226	1	ATP6_MACRO	P92664 macropus r.
45	76	6.9	463	1	Y096_MYCTU	Q10892 mycobacteri

ALIGNMENTS

RESULT	1	STANDARD	PRT	182 AA.
PLP_HUMAN				
ID	PLP_HUMAN			
AC	09Y342			
DT	01-OCT-2000 (Rel. 40, Created)			
DT	01-OCT-2000 (Rel. 40, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	PLASMOLOPIN.			
OS	Homo sapiens (Human).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid:9606;			
NP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-Kidney;			
RA	Xie B., Durrle R., Sapirstein V.S.;			
RT	"Molecular cloning of human plasmolipin cDNA."			
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: APPEARS TO BE INVOLVED IN MYELINATION. COULD ALSO PARTICIPATE IN ION TRANSPORT EVENTS AS ADDITION OF PLASMOLOPIN TO LIPID BILAYERS INDUCES THE FORMATION OF ION CHANNELS, WHICH ARE VOLTAGE-DEPENDENT AND K(+)-SELECTIVE (BY SIMILARITY).			
CC	-1- SUBUNIT: HEXAMER ARRANGED AS A TRIMER OF TWO PLASMOLOPIN SUBUNITS (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: BELONGS TO THE MAL FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
DR	EMBL; AF137386; AAD33060.1;			
DR	Tranmembrane; Transport; Ionic channel; Ion transport.			
KM	DOMAIN 1			
FT	DOMAIN 1			
FT	TRANSSEM 36			
FT	TRANSSEM 57			
FT	DOMAIN 69			
FT	TRANSSEM 90			
FT	DOMAIN 100			
FT	TRANSSEM 121			
FT	DOMAIN 141			
FT	TRANSSEM 162			
FT	DOMAIN 182			
SO	SEQUENCE 182 AA; 19986 MW; 6809AA080E2P67EB CRC64;			

Query Match 84.5%; Score 930; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 9.6e-63;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MAEPFSKYSTRSSPAQGAEEVSALRPDLGPFVSRSLAKMLQVLGLWALIAADPPY 60
|||||

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 CC or send an email to license@sib-sib.ch).
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 DR EMBL; Y07812; CAA69143.1; -
 DR MGD; MGI:892970; Mal.
 KM Transmembrane; Lipoprotein; Myelin.
 FT DOMAIN 1 24 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 25 46 POTENTIAL.
 FT DOMAIN 47 53 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 54 75 POTENTIAL.
 FT DOMAIN 76 92 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 93 114 POTENTIAL.
 FT DOMAIN 115 125 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 126 147 POTENTIAL.
 FT DOMAIN 148 153 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 153 AA; 16595 MW; 5EED415344669B4B CRC64;

Query Match 14.1%; Score 155; DB 1; Length 153;
 Best Local Similarity 32.7%; Pred. No. 2.7e-05;
 Matches 48; Conservative 21; Mismatches 64; Indels 14; Gaps 4;

OY 22 SVSALRPDLGFVRSRIGALMLDLVGLVLMALADT--PYHLRYAYGVNMFVAFLMLV 81
 DB 17 SVFTTLPDLFV-----CEFFVGGVLTLLVSLVPLAOCGVNMFVFCVAVT 67
 OY 82 VFENLYLQHLKLYMPVPLVIMFNISATVLYTAFIAGSAVDTSLRG--TRPYNO 139
 DB 68 SLMTLYITGTHGG--ETSHITLDAAYHCVALLFTLSASV--LEALATISMFDGFTYKHHE 124
 OY 140 RAASAFACLVMIAYGVSAFESYQAMR 166
 DB 125 NIAAVFAVYVTLIYVHAVFSLIRMK 151
 RESULT 4
 MAL_HUMAN STANDARD; PRT; 153 AA.
 ID MAL_HUMAN
 AC P21145;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE MYELIN AND LYMPHOCYTE PROTEIN (T-LYMPHOCYTE MATURATION-ASSOCIATED
 DE PROTEIN).
 GN MAL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=87175600; PubMed=3494249;
 RA Alonso M.A., Weissman S.M.;
 RT "cDNA cloning and sequence of MAL, a hydrophobic protein associated
 RT with human T-cell differentiation.";
 RT Proc. Natl. Acad. Sci. U.S.A. 84:1997-2001(1987).
 RP SEQUENCE FROM N.A.
 RP TISSUE=Lymphocytes, and Placenta;
 RA MEDLINE=94179190; PubMed=8132541;
 RA Rancano C., Rubio T., Cortes I., Alonso M.A.;
 RT "Genomic structure and subcellular localization of MAL, a human
 RT T-cell-specific proteolipid protein.";
 RT J. Biol. Chem. 269:8159-8164(1994).

RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94375076; PubMed=8088843;
 RA Rancano C., Rubio T., Alonso M.A.;
 RT "Alternative splicing of human T-cell-specific MAL mRNA and its
 RT correlation with the exon/intron organization of the gene.";
 RL Genomics 21:447-450(1994).
 CC -1- FUNCTION: COULD BE AN IMPORTANT COMPONENT IN VESICULAR TRAFFICKING
 CC CYCLING BETWEEN THE GOLGI COMPLEX AND THE APICAL PLASMA MEMBRANE.
 CC COULD BE INVOLVED IN MYELIN BIOGENESIS AND/OR MYELIN FUNCTION.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; A (SHOWN HERE), B, C AND D; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE INTERMEDIATE AND LATE
 CC STAGES OF T-CELL DIFFERENTIATION.
 CC -1- PIM: LIPOPROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE MAL FAMILY.
 CC -----
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 CC -----

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 DR E

RESULT 5
MAL_RAT STANDARD; PRT; 153 AA.
AC 064349;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE MYELIN AND LYMPHOCYTE PROTEIN (T-LYMPHOCYTE MATURATION-ASSOCIATED
DE PROTEIN) (17 KDA MYELIN VESICULAR PROTEIN) (MVP17) (NS 3).
GN MAL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=Brain;
RA MEDLINE=96123965; PubMed=9583510;
RA Kim T., Fiedler K., Madison D.L., Krueger W.H., Pfeiffer S.E.;
RT "Cloning and characterization of MVP17: a developmentally regulated
RT myelin protein in oligodendrocytes";
RL J. Neurosci. Res. 42:413-422(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LEWIS; TISSUE=Spinal cord;
RA MEDLINE=95370938; PubMed=7643216;
RA Characterization of a rat gene, RML, encoding a protein with four
RT hydrophobic domains in central and peripheral myelin.";
RL J. Neurosci. 15:5753-5764(1995).
CC -1- FUNCTION: COULD BE AN IMPORTANT COMPONENT IN VESICULAR TRAFFICKING
CC CYCLING BETWEEN THE GOLGI COMPLEX AND THE APICAL PLASMA MEMBRANE.
CC COULD BE INVOLVED IN MYELIN BIOGENESIS AND/OR MYELIN FUNCTION.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXCLUSIVELY EXPRESSED IN WHITE AND GRAY MATTER
CC OLIGODENDROCYTES IN THE CNS AND IN MYELINATING SCHWANN CELLS IN
CC PERIPHERAL NERVES. HIGHER LEVELS ARE FOUND IN THE WHITE. WEAK
CC CNS OR SPINAL CORD. IN THE GRAY MATTER THAN IN THE WHITE.
CC EXPRESSION ALSO FOUND IN SPLEEN AND KIDNEY.
CC -1- DEVELOPMENTAL STAGE: DETECTED JUST BEFORE BIRTH IN SCHWANN CELLS
CC AND AFTER BIRTH IN OLIGODENDROCYTES OF BRAINSTEM AND SPINAL CORD.
CC -1- INDUCTION: UPREGULATED DURING MYELINATION.
CC -1- PM: LIPOPROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE MAL FAMILY.
CC -----
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CC -----
DR EMBL; U13367; AAC52366.1; -
DR EMBL; X82557; CA837903.1; -
FT Transmembrane; Lipoprotein; Myelin.
FT DOMAIN 1 24
FT TRANSSEM 25 46
FT TRANSSEM 47 53
FT TRANSSEM 54 75
FT TRANSSEM 76 92
FT TRANSSEM 93 114
FT TRANSSEM 115 125
FT TRANSSEM 126 147
FT TRANSSEM 148 153
FT DOMAIN 153 AA; 16758 MM; C98996DC3612494 CRC64;
SO SEQUENCE

Query Match 13.8%; Score 152; DB 1; Length 153;
Best Local Similarity 29.9%; Pred. No. 4.6e-05;
Matches 44; Conservative 23; Mismatches 66; Indels 14; Gaps 4;

OY 22 SVSALRPDLGVRSRRLGALMLQVLVALLADPPYHLYPAVGWYFVAPLAVTI 81
DB 17 SVFTFDPDL-----LFFEFIFGGLVWILLASSLPVGVGVVSVCEFLATT 67
OY 82 VLFNLYFQGLMKRYMPWPLVLMIFNLSATVLTAFIACSAVDLSLNG--TRPNO 139
DB 68 SLAWMTIIGHGG--ETSMITLDAAVHCVAALFTLSASV-LEALATTWFDGFTYRYHE 124
OY 140 RAASAFACLVMIYGVSAFESYOAMR 166
DB 125 NIAAVFAVATLLYHVAVSLRMK 151
RESULT 6
BENE_HUMAN STANDARD; PRT; 148 AA.
AC 013021;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE BENE PROTEIN (FRAGMENT).
GN BENE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=95347597; PubMed=7622049;
RA Lautner-Rieske A., Thiede R., Zachau H.G.;
RT "Searching for non-v kappa transcripts from the human immunoglobulin
RT kappa locus.";
RL Gene 159:199-202(1995).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE MAL FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U17077; AAA6738.1; -
DR MIM; 602222; -
FT Transmembrane 1
FT NON_TER 1
FT TRANSSEM 17 37
FT TRANSSEM 37 74
FT TRANSSEM 54 74
FT TRANSSEM 92 112
FT TRANSSEM 126 146
FT TRANSSEM 148 AA; 16849 MM; 561955796EE78DAB CRC64;
SO SEQUENCE

Query Match 13.5%; Score 148.5; DB 1; Length 148;
Best Local Similarity 30.2%; Pred. No. 8.1e-05;
Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;

OY 39 ALMLDQVLGLVALLADPPYHLYP-AYGVWVAVFVLTIVLPLVLFQGLMKLYM 97
DB 24 AFLPLDLFFGLVLTWVAAT-HIYPLDQGVWVVSLSFLISLFTLSYFGFYKR--F 80
OY 98 VPMPLVIMNISATVLYIT-AFIACSAVDLTSRGTRPNORAAAFACLVMIYGV 156
DB 81 ESRWVDSLHGTGIIYMAAVYQVATVSEKLDPRITTYINSASFPAITLITIL 140
OY 157 SAFFSY 162
DB 141 HAFSIV 146

RESULT	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528</
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DT 01-Oct-2000 (Rel. 40, Last annotation update)
DE MYELOID-ASSOCIATED DIFFERENTIATION MARKER (MYELOID UPREGULATED
GN MYADM OR MDG.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Euteria; Rodentia; Sclurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN
  [1]
  SEQUENCE FROM N.A.
  Pettersson M., Nilsson K., Jonsson J.I.;
  Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.
  -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
  -1- SIMILARITY: BELONGS TO THE MAL FAMILY.
  -----
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  -----
  CC EMBL; AJ001616; CA04870.1;
  DR MGD; MGI:1355332; Myadm.
  KM Transmembrane.
  FT Transmem 35 55 POTENTIAL.
  FT TRANSMEM 61 81 POTENTIAL.
  FT TRANSMEM 95 115 POTENTIAL.
  FT TRANSMEM 131 151 POTENTIAL.
  FT TRANSMEM 166 186 POTENTIAL.
  FT TRANSMEM 197 217 POTENTIAL.
  FT TRANSMEM 225 245 POTENTIAL.
  FT TRANSMEM 263 283 POTENTIAL.
  SQ SEQUENCE 296 AA; 32098 MW; 5BD37C839734AD9D CRC64;

Query Match 11.9%; Score 131; DB 1; Length 296;
Best Local Similarity 25.4%; Pred. No. 0.0029;
Matches 45; Conservative 28; Mismatches 76; Indels 28; Gaps 6;

QY 8 VSTRSSPAQGAEASVASRPDLGFVRSRLGALMLLQVLYGLLWMLINDFRPHYLPAVG 67
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  10 ITTTSSSR--TVGSAKALTOPLEGILR-----LLQLISTCVASPLSVAGAMCPKMN 60
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 68 WYWEAVAFPLMYLYIVLEFNLYL--FOLHMKLYMPWPLVY---MFPNISATVLYTAFIA 121
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 WAMFTWCFENATVLLILLYELGSLAHPFLSMKNPFITFACVAALECLSSITPTTY- 119
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 122 CSAANDJLSKRGTRPYNCPAASFPACLYMIAVGSAFPSYQAMRGVGSNAATSOQA 178
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 120 -----CPLAGRGRTDHAIAAATTSVCVACLAVATEV-----AMTRARPGEITGYMA 164
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
ID NOST_PSEST STANDARD; PRT; 276 AA.
AC P19845;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1992 (Rel. 21, Last annotation update)
OS MEMBRANE PROTEIN NOST PRECURSOR.
DE Pseudomonas stutzeri (Pseudomonas perfectomarina).
CC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
CC Pseudomonas.
OX NCBI_TaxID=316;
RN
  [1]
  SEQUENCE FROM N.A.
  RC STRAIN=ATCC 14405 / ZOBELL;
  RC MEDLINE=91006150; PubMed=2170125;
  RA Zunft W.G., Viebrock-Sambale A., Braun C.;
  RT Nitrous oxide reductase from denitrifying Pseudomonas stutzeri.
  Genes for copper-processing and properties of the deduced products,

```

RT including a new member of the family of ATP/GTP-binding proteins.";
 RL Eur. J. Biochem. 193:591-599(1990).
 CC -1- FUNCTION: INVOLVED IN COPPER PROCESSING.
 CC -1- SUBCELLULAR LOCATION: PLASMA MEMBRANE.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X53676; CA37717.1; -
 DR PIR: S13585; S13585.
 KW Transmembrane; Copper; Signal.
 FT SIGNAL 1 34
 FT CHAIN 35 276 MEMBRANE PROTEIN NOSY.
 SQ SEQUENCE 276 AA; 29434 MW; 91411E4F0AD8D5 CRC64;

Query Match 8.6%; Score 95; DB 1; Length 276;
 Best Local Similarity 24.3%; Pred. No. 1.3;
 Matches 43; Conservative 31; Mismatches 55; Indels 48; Gaps 9;

OY 23 VSALRPDGFVRSRLGALMLQLV-LGLVWA-----LADTPHYHYRAYGVNF----- 71
 DB 111 IIALVLVLFQFCALALVLEGVGLVLFVAFGRFMIST-----LLGVVLAFAVYL 164
 OY 72 -----VAFLVLTIVLENTLFLQL-----HMLVYVMPVLMIFINISATV 113
 DB 165 SGKVKESKSSAGLALGVFLVIVFDVLLVLLVLSSEKFMPELLPILL-----NPTD 219
 OY 114 LY-----ITAFIACSAAVDLTSLGRTPYNOAASFACLVMIYGVSAFESYQAMR 166
 DB 220 IYRLINISGFESGSSAMGVLSIGADLPV---PAAVLMCL-LAMIGVSLIAYIAFR 272

RESULT 10
 GLTS_ECOLI STANDARD; PRT; 401 AA.
 AC P19933;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE SODIUM/GLUTAMATE SYMPORT CARRIER PROTEIN (GLUTAMATE PERMEASE).
 GN GLTS OR GLTC.
 OS Escherichia coli.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Escherichia.
 OX NCBI_TaxID:562;
 OX [1]
 RN RN
 RP SEQUENCE FROM N.A.
 RC STRAIN-B:
 RX MEDLINE-91072371; PubMed-2254324;
 RA Deguchi Y., Yamato I., Anraku Y.,
 RT "Nucleotide sequence of glts, the Na⁺/glutamate symport carrier gene
 of Escherichia coli B.";
 RL J. Biol. Chem. 265:21704-21708(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE-91203811; PubMed-2017136;
 RA Kalman M., Gentry D., Cashel M.,
 RT "Characterization of the Escherichia coli K12 glts glutamate permease
 gene.";
 RL Mol. Gen. Genet. 225:379-386(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE-93315143; PubMed-7686882;
 RA Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
 RT "DNA sequence and analysis of 136 kilobases of the Escherichia coli

RT genome: organizational symmetry around the origin of replication.";
 RL Genomics 16:551-561(1993).
 CC [4]
 RP SEQUENCE OF 379-401 FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE-92184121; PubMed-1544582;
 RA Kalman M., Murphy H., Cashel M.,
 RT "The nucleotide sequence of recg, the distal spo operon gene in
 Escherichia coli K-12.";
 RL Gene 110:95-99(1992).
 CC -1- FUNCTION: CATALYZES THE SODIUM-DEPENDENT UPTAKE OF EXTRACELLULAR
 CC GLUTAMATE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
 CC -----
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 CC -----
 DR EMBL: D00626; BAA00517.1; -
 DR EMBL: X17499; CA35540.1; -
 DR EMBL: L10328; AAA62006.1; -
 DR EMBL: AE000442; AAC76677.1; -
 DR EMBL: M6367; AAA28514.1; -
 DR PIR: J00489; YOECONO.
 DR PIR: A36524; A36524.
 DR PIR: S14031; S14031.
 DR Ecogene: EG10406; glts.
 KW Transport; Transmembrane; Inner membrane; Sodium transport; Symport.
 FT TRANSMEM 3 21 POTENTIAL.
 FT TRANSMEM 36 54 POTENTIAL.
 FT TRANSMEM 69 87 POTENTIAL.
 FT TRANSMEM 91 109 POTENTIAL.
 FT TRANSMEM 112 132 POTENTIAL.
 FT TRANSMEM 160 178 POTENTIAL.
 FT TRANSMEM 214 240 POTENTIAL.
 FT TRANSMEM 246 267 POTENTIAL.
 FT TRANSMEM 276 294 POTENTIAL.
 FT TRANSMEM 301 325 POTENTIAL.
 FT TRANSMEM 336 357 POTENTIAL.
 FT TRANSMEM 371 398 POTENTIAL.
 FT CONFLICT 378 378 G -> S (IN REF. 1).
 SQ SEQUENCE 401 AA; 42425 MW; 9569AE0AF7634DC CRC64;

Query Match 8.6%; Score 95; DB 1; Length 401;
 Best Local Similarity 22.6%; Pred. No. 1.7;
 Matches 47; Conservative 35; Mismatches 96; Indels 30; Gaps 6;

OY 1 MAERPSKVSRTSSPAGAEASVALRPDGFVSRG-----ALMLQLVGLVWALI 55
 DB 179 VAVLVHSTPNIPDDQEVPAFEKPDVGRMTSLVLETTIALMLCLVGVIVQL 238
 OY 56 ADPEHYLPYAGVWVFAVFLMTIVLENTLFLQLHMKLVVMPVLMIFINISATV 115
 DB 239 AGTAFEL-PFVCLVLFVGLISNGLSI-----MGFVRYERAVSVYGNVSLIFL 287
 OY 116 ITAFIACSAAVDLTSLGRTPYNOAASFACLVMIYGVSAFESYQAMR 175
 DB 288 AMLMGLK-LWEIASL-----ALPMLAIIVQITIFALYAIPTWBMGKNYDAA 336
 OY 176 QMAGVATTCATAPSGAAGSRYT 203
 DB 337 VLAAGH---CGFGIGATPTAIANMOAIT 361

RESULT 11
 A4P_HUMAN STANDARD; PRT; 152 AA.
 ID A4P_HUMAN
 AC Q04941;

[illegible]

ID	NAME	STANDARD	PROT	444 AA
AC	XX HUMAN			
AC	XX HUMAN	STANDARD	PROT	444 AA
AC	P51811			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	MEMBRANE TRANSPORT PROTEIN XK (KX ANTIGEN).			
GN	XX			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_Taxid:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-94273191; Pubmed-8004674;			
RA	Ho M., Chelly J., Carter N., Danev A., Crocker P., Monaco A.P.;			
RT	"Isolation of the gene for McLeod syndrome that encodes a novel			
RL	membrane transport protein."			
RN	Cell 77:869-880(1994).			
RP	[2]			
RA	REVIEWS TO 204-205.			
RL	Ho M.F.;			
CC	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.			
CC	-1 FUNCTION: MAY BE INVOLVED IN SODIUM-DEPENDENT TRANSPORT OF NEUTRAL			
CC	AMINO ACIDS OR OLIGOPEPTIDES.			
CC	-1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).			
CC	-1 TISSUE SPECIFICITY: HIGH LEVELS IN SKELETAL MUSCLE, HEART, BRAIN,			
CC	AND PANCREAS; LOW LEVELS IN PLACENTA, LUNG, LIVER, AND KIDNEY.			
CC	-1 POLYMORPHISM: XK IS RESPONSIBLE FOR THE KX BLOOD GROUP SYSTEM.			
CC	-1 DISEASE: DEFECTS IN XK ARE THE CAUSE OF MCLEOD SYNDROME, AN X-			
CC	LINKED MULTISYSTEM DISORDER CHARACTERIZED BY ABNORMALITIES IN THE			
CC	NEUROMUSCULAR AND HEMATOPOIETIC SYSTEMS.			
CC	-----			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; 232684; CAA83632.1; -			
DR	MI; 314850; -			
FM	Transmembrane: Transport; Amino acid transport; Blood group antigen.			
FT	DOMAIN 1			
FT	TRANSMEM 2			
FT	TRANSMEM 3			
FT	DOMAIN 24			
FT	TRANSMEM 37			
FT	TRANSMEM 38			
FT	DOMAIN 59			
FT	TRANSMEM 69			
FT	TRANSMEM 89			
FT	DOMAIN 90			
FT	TRANSMEM 140			
FT	TRANSMEM 141			
FT	DOMAIN 162			
FT	TRANSMEM 171			
FT	TRANSMEM 172			
FT	DOMAIN 193			
FT	TRANSMEM 208			
FT	TRANSMEM 209			
FT	DOMAIN 230			
FT	TRANSMEM 235			
FT	TRANSMEM 236			
FT	DOMAIN 257			
FT	TRANSMEM 277			
FT	TRANSMEM 278			
FT	DOMAIN 299			
FT	TRANSMEM 317			
FT	TRANSMEM 318			
FT	DOMAIN 338			
FT	TRANSMEM 349			
FT	TRANSMEM 350			
FT	TRANSMEM 370			
FT	DOMAIN 371			
SO	SEQUENCE 444 AA; 50876 MW; E94BDD0E3BEF7AB2 CnC64;			

Query Match 8.5%; Score 93.5; DB 1; Length 444;
Best Local Similarity 22.4%; Pred. No. 2.4;
Matches 39; Conservative 28; Mismatches 66; Indels 41; Gaps 8;

13 SSPAGAGAAASVSAALPDPDGFVNSRGALMLDLVLGLVLAALIA-DTPHLYPA-YGWTM 70


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Db 148 SAPOLITOLLYISMAQODPTVGRSLILMTISLISLYYALRCNIIAIIKIKYDEYEVKVALA 207
QY 71 FVAVEIM-----LVYIVFNLYLXFLQHNKKLYMWPPLVLMFNISAVLVITAFIAC 1223
Dd 208 IYCIJFLMSFEIATRVAVLVLETSVL-----KTMVVVILLIINFSFLLPMLIEMWC 258
QY 123 SAAVDLTLNSTRBRYNO-----RAAASFACLVMIAY-GVSAFESQYAMRGV 168
Dd 259 SGS-----PFPENIEKALSRVCTIYLCVLTILLYIGINNF-----CMSAV 298

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RESULT 13

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ID SMVA_SALT1 STANDARD; PRT; 496 AA.
AC P37594;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE METHYL VIIOLOGEN RESISTANCE PROTEIN SMVA.
GN SMVA.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SL1303;
RC MEDLINE=95011654; PubMed=7926834;
RA Hongo E., Moriyo M., Mita K., Machida I., Hama-Iraba H., Tsuji H.,
RA Ichimura S., Noda Y.;
RT "The methyl viologen-resistance-encoding gene smva of Salmonella
RT typhimurium ";
RL Gene 148:173-174(1994).
CC -1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
CC (POTENTIAL).
CC -1 SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN
CC AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).
-----
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Db 195 LGHVMMILIALILLVYSAKTALKGLH-----SLWVISYTLTGALLGFIPT 242
Oy 90 OLHKLYVWPMPVLYLMTFNISATVLYITAFACSA-----AVDLSLGRPRPNORAAAS 144
Db 243 QLATSRPMIDNRLEFTHRIILSGVMMAMTITLVGFELMAOELQFPHGSPYE---AG 298
Oy 145 FFACLYMAYAVGS-----AFFSYQAMRG--- 167
Db 299 VFMLPVWYASQFSPPIAGVIVSRGLRLVATGMAISALSIFYGLAMTDFSTQOQAWGLM 358
Oy 168 --VGSNAATSOMAGGYATTCTATGSGAEAAAGSOSRYTLASWGLRGVS 215
Db 339 ALIGFSNASSALIA---STSAITMAAPPEKAAAGAITMAVEIGAGGICIA 405

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RESULT 14

ID LMP1_EBYC STANDARD; PRJ: 404 AA.
 AC P29362;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sentence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE LATENT MEMBRANE PROTEIN 1 (LMP-1) (P63).
 GN BNLF1.
 OS Epstein-Barr virus (strain Cao) (Human herpesvirus 4).
 CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC Gammaherpesvirinae; Lymphocryptovirus.
 CC NCBI_TaxID=31525;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92013956; PubMed=1681026;
 RA Hu L.F., Zadorovskiy E.R., Chen F., Cao S.L., Ernberg I., Klein G.,
 RA Winberg G.;
 RT "Isolation and sequencing of the Epstein-Barr virus BNLF-1 gene
 (LMP1) from a chinese nasopharyngeal carcinoma.";
 RL J. Gen. Virol. 72:2399-2409(1991).
 CC -1- FUNCTION: THE LATENT MEMBRANE PROTEIN HAS TRANSFORMING ACTIVITY.
 CC -----
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 CC -----
 CC

QY 130 SLRGTREYNQAAAFACLVMIAYGVSAPFSYQAWR 166
DB 114 -----EGCL--LVEGIMTYFFLETLMR 132

RESULT 15

B3AR_RAT STANDARD; PRT; 400 AA.

AC P26255;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE BETA-3 ADRENERGIC RECEPTOR.
GN ADRB3 OR ADRB3R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RX MEDLINE=92084710; PubMed=1721063;
RA Muzza P., Revelli J.-P., Kuhne F., Gocayne J.D., McCombie W.R.,
RA Venter J.C., Giacobino J.-P., Fraser C.M.;
RT "An adipose tissue-specific beta-adrenergic receptor. Molecular
RT cloning and down-regulation in obesity."
RT J. Biol. Chem. 266:24053-24058(1991).
RN [2]
RX MEDLINE=92100057; PubMed=1684635;
RA Granneman J.G., Labners K.N., Chaudhry A.;
RT "Molecular cloning and expression of the rat beta 3-adrenergic
RT receptor."
RT Mol. Pharmacol. 40:895-899(1991).
RN [3]
RX MEDLINE=93178631; PubMed=8382630;
RA Bensaïd M., Kaghad M., Rodriguez M., le Fur G., Caput D.;
RT "The rat beta 3-adrenergic receptor gene contains an intron."
RT FBS Lett. 318:223-226(1993).
CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
PROTEINS. BETA-3 IS INVOLVED IN THE REGULATION OF LIPOLYSIS AND
THERMOGENESIS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: WHITE AND BROWN ADIPOSE TISSUES, AND DIGESTIVE
TRACT.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC EMBL: M74716; AAA74470.1; -
CC EMBL: S73473; AAB20702.1; -
CC EMBL: S56481; AAB25520.1; -
CC EMBL: S56152; AAB25521.1; -
CC PIR: A41679; A41679.
CC PIR: S29808; S29808.
CC PIR: A53281; A53281.
CC HSSP: P07700; 1DER.
CC GCRDB: GCR_0287; -
CC GCRDB: GCR_0622; -
CC GCRDB: GCR_0732; -
CC InterPro: IPR000276; -
CC InterPro: IPR000681; -
CC InterPro: IPR002233; -
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS: PR00237; GPCRHHODPSN.

DR PRINTS: PR00563; ADRENGCB3AR.
DR PRINTS: PR01103; ADRENGICR.
DR PROSITE: PS00237; G-PROTEIN_RECIP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECIP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 36
FT TRANSMEM 37 60
FT DOMAIN 61 69
FT TRANSMEM 70 88
FT DOMAIN 89 108
FT TRANSMEM 109 130
FT DOMAIN 131 152
FT TRANSMEM 153 175
FT DOMAIN 176 200
FT TRANSMEM 201 222
FT DOMAIN 223 289
FT TRANSMEM 290 311
FT DOMAIN 312 323
FT TRANSMEM 324 344
FT DOMAIN 345 400
FT CARBOHYD 8 26
FT CARBOHYD 107 186
FT DISULFID 107 186
FT LIPID 358 358
FT CONFLICT 234 235
SQ SEQUENCE 400 AA; 43146 MW; D588540C4BCEB13 CRC64;

Query Match 7.9%; Score 86.5; DB 1; Length 400;
Best Local Similarity 26.8%; Pred. No. 7.3;
Matches 55; Conservative 31; Mismatches 70; Indels 49; Gaps 11;

QY 1 MAEPPSK---VSTRSSPQAGAEASVSALRPDLGFVSRIGALMLDLVIG-LVVMALIA 56
DB 1 MAPPHKNGSLAFMSDAPTLDPSSAANTSGLGVPMAAALAGALLATVGGNLLVITATA 60
QY 57 DTPHLLPAIGVWVFVFLMLVTVIVLENLYFQHLKLVVNP-----WPLYMT 106
DB 61 RTRP-----LQITVVFVTSLATVADLVGLVMPGATLALTGHPPLGATG 106
QY 107 ENI--SATVLYITAFI--ACSAVD-----LTSIR-GTRPNQORAAAFACLVMIAYGV 156
DB 107 CELMTSDVCLVTASIEFLCALADRYLATVNPRLIGTLTKRRARA-----VVLWIV 161
QY 157 SAFSYY-----QAMRGVSNATSQ 176
DB 162 SATVSFAPINQSMWR-VGADAAQAE 185

Search completed: May 2, 2001, 15:11:39
Job time: 79 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 2, 2001, 15:09:56 ; Search time 22.67 Seconds
(Without alignments)
1116,758 Million cell updates/sec

Title: US-09-602-597-4
Perfect score: 1101
Sequence: 1 MAEPFSKVSRTSSPAOGAE.....GSOSRYTLQASWGLRGVSP 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mmc:
8: sp-organelle:
9: sp-phage:
10: sp-plant:
11: sp-rodent:
12: sp-unclassified:
13: sp-vertebrate:
14: sp-virus:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	930	84.5	182	4	Q9Y342
2	158	14.4	281	5	001539
3	137	12.4	177	5	09VZ71
4	104.5	9.5	152	11	09R107
5	93	8.4	471	2	09JVA3
6	93	8.4	610	5	044986
7	93	8.4	693	10	09LK50
8	92	8.4	471	2	09R032
9	91	8.3	208	5	021228
10	91	8.3	379	2	09K1T9
11	91	8.3	415	2	092739
12	90.5	8.2	273	2	068480
13	90.5	8.2	461	10	09M100
14	90	8.2	401	10	040568
15	90	8.2	539	2	045577
16	89	8.1	238	14	09Y0Y5
17	89	8.1	264	2	034535
18	89	8.1	417	5	09Y0K9
19	88.5	8.0	215	2	09K8Y7

20	88.5	8.0	244	5	020241	Q02041 caenorhabd
21	88.5	8.0	429	2	09RUV8	Q9RUV8 deinococcus
22	88.5	8.0	3005	14	056074	Q56074 hepatitis g
23	88	8.0	331	5	093869	Q93869 caenorhabd
24	87.5	7.9	229	8	0939P1	Q939P1 terebratul
25	87.5	7.9	464	2	09RYX1	Q9RYX1 deinococcus
26	87.5	7.9	1192	10	09S770	Q9S770 arbidops
27	87	7.9	122	8	003762	Q03762 pediatrum
28	87	7.9	160	5	09YTX8	Q9YTX8 drosophila
29	87	7.9	506	5	023576	Q23576 caenorhabd
30	86.5	7.9	212	8	079613	Q79613 rusaia ros
31	86	7.8	344	2	09XDA1	Q9XDA1 thermom
32	86	7.8	406	5	044990	Q44990 caenorhabd
33	86	7.8	449	2	045082	Q45082 burkholderi
34	85.5	7.8	519	5	009592	Q09592 caenorhabd
35	85	7.7	338	2	09KX69	Q9KX69 streptomy
36	85	7.7	358	2	P77568	P77568 pseudomon
37	85	7.7	516	2	053508	053508 mycobacteri
38	85	7.7	999	9	021882	Q21882 bacterioph
39	85	7.7	1083	4	09Y666	Q9Y666 homo sapien
40	85	7.7	1147	2	09KVS4	Q9KVS4 vibrio chol
41	84.5	7.7	314	2	09YXF8	Q9YXF8 neisseria m
42	84.5	7.7	397	1	027735	027735 methanobact
43	84.5	7.7	405	2	09RJ60	Q9RJ60 streptomy
44	84.5	7.7	419	2	087601	Q87601 streptomyc
45	84.5	7.7	467	6	09TT96	Q9TT96 bos taurus

ALIGNMENTS

RESULT 1
ID Q9Y342 PRELIMINARY; PRT; 182 AA.
AC Q9Y342;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE PLASMOLOPIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RA Xie B., Durrie R., Sapirstein V.S.;
RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF137386; AAD33060.1;
SQ SEQUENCE 182 AA; 19986 MW; 6F09AA080E2F67E8 CRC64;

Query Match 84.5%; Score 930; DB 4; Length 182;
Best Local Similarity 100.0%; Pred. NO. 2.3e-64;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEPFSKVSRTSSPAOGAEASVSALRPDLGFVRSRLGALMLQIVLGLVVALADDPY 60
DB 1 MAEPFSKVSRTSSPAOGAEASVSALRPDLGFVRSRLGALMLQIVLGLVVALADDPY 60
QY 61 HLYPAVGWVFAVFLMLVTIVLFNLVLEQLHMKLYMPWPLVLMIFNISATVLYTAFI 120
DB 61 HLYPAVGWVFAVFLMLVTIVLFNLVLEQLHMKLYMPWPLVLMIFNISATVLYTAFI 120
QY 121 ACSAAVDLSLGTTPRYNRAAASFFACLYMAYGVSAFSGQARVGCSNAATSQMAGG 180
DB 121 ACSAAVDLSLGTTPRYNRAAASFFACLYMAYGVSAFSGQARVGCSNAATSQMAGG 180
QY 181 VA 182
DB 181 VA 182

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RESULT 2
ID 001539 PRELIMINARY; PRT; 281 AA.
AC 001539;
DE 01-JUL-1997 (TREMBLrel. 04, Created)
DE 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE 01-JUL-2000 (TREMBLrel. 14, Last annotation update)
DE 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CG15211 PROTEIN.
GN F28H1.4 OR F47B3.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Lalster N., Latreille P.,
RA Lightfoot J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Ritten L., Roopra A., Saunders D., Showman R.,
RA Smailson D., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thelery-Mleg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstein L., Wilkinson-Sproat J., Wohlman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX Du Z., Le T.T.;
RA Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U97013; AAB52340.1;
DR EMBL: U97017; AAB52358.1;
DR EMBL: 281 AA; 31473 MW; CB2007649B/DA573 CRC64;
SQ
Query Match 14.4%; Score 158; DB 5; Length 281;
Best Local Similarity 28.6%; Pred. No. 5; le-05;
Matches 50; Conservative 27; Mismatches 76; Indels 22; Gaps 5;
QY 18 GAASVSALRPDLGFRSRLGALMLDLVLGALVALLADTPYHLRYAGWMAVAVFLW 77
DB 104 GPAVIEPRDCEYIRFLGIMKIVICVLCCLFIFVPMGPAY-YGVGWAATVSSVGI 162
QY 78 LVTLYLFNLYFOLMKIKYMPPLVY-----MIRINATYLYITAFACSAAY 126
DB 163 FVTYSLTLTYFRVVDLPSTINWVCLSTREITIIIDEMVYCFAMTVFFFLA--ACVLA 220
QY 127 DLTSLAGTRPNORAAAFACLVIAVAGVSAFYSQAMRG-----GSMNATSQ 176
DB 221 ASSQGRGFAM---AIAFAFGACAGFPCYIKFLSKNNKRAATGGSNPNVVIQ 272
RESULT 3
Q9VZ71 PRELIMINARY; PRT; 177 AA.
AC 09VZ71;
DE 01-MAY-2000 (TREMBLrel. 13, Created)
DE 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CG15211 PROTEIN.
GN CG15211.
OS Drosophila melanogaster (Fruit fly).

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OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan R.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Adair J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burlis K.C., Busam D.A., Butler J., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodes A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitai M., Kalush F., Kapran G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Irel Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zibds R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003484; AAF47955.1;
DR FLYBASE: FBgn0030234; CG15211.
SQ SEQUENCE 177 AA; 18910 MW; ED40DBA6B8BD1D41 CRC64;
QY 9 STRTSSPAQGAESV-----SALRPDLGFRSRLGALMLDLVLGALVALLADTPYH 61
DB 13 TTTTNGPPGAGNPVSGSGGFWSAIRLNIDYFRIPGIKIVKIVKIVKIVKIVKIVKIV 69
QY 62 LYPAYGVVMAVAVFLVLTLYLFNLYFOLMKIKYMPPLVY-----MIRINATYLYITAF 120
DB 70 LASATSEFMFVYIVTSIFILLINLAAYLGLREALNVAVNMFTSELTITTAVALTLTYFGFI 129
QY 121 ACSAAVDLTSLAGTRPNORAAAFACLVIAVAGVSAFYSQAMR 166
DB 130 VQLAWSMDATGKS---GSNTAGVDFGLFNLALAAAGTYFLFLHR 172
RESULT 4
Q9RI07 PRELIMINARY; PRT; 152 AA.
AC 09RI07;
DE 01-MAY-2000 (TREMBLrel. 13, Created)

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DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE PROTEOLIPID PROTEIN 2.
 GN PLP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hayashi A., Hattori A., Okaze H., Kozuma S., Seki N., Satto T.;
 RT "Mouse proteolipid protein 2 (PLP2)."
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB031292; BAA83500.1; -
 SO SEQUENCE 152 AA; 16607 MW; C651A5E43B2909D6 CRC64;

Query Match 9.5%; Score 104.5; DB 11; Length 152;
 Best Local Similarity 22.9%; Pred. No. 0.38;
 Matches 30; Conservative 26; Mismatches 60; Indels 15; Gaps 3;

OY 32 EVSRRLGALMLQLVGLLWALLADPYHLYPAYGWFVAVFLVTLVFNLYLFEOL 91
 DB 19 FSRTKRGILLFAEIIICLVILICFSASTSAYSS-----LSVTEMICAAVLVFTCDL 72
 OY 92 HMKLVVPPPLVIMINISATVYITAFACSAVDLSRGTRPTNORAAAFACLVW 151
 DB 73 HSKISFNPMPWDFRSLTATILYITSTI-----VVLVEGRG-----SSRVAGIIGLLAT 123
 OY 152 IAVGSAFFSY 162
 DB 124 LFGYDAITTF 134

RESULT 5
 O9JY43 PRELIMINARY; PRT; 471 AA.
 AC O9JY43:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE PUTATIVE TRANSMEMBRANE TRANSPORT PROTEIN.
 GN NMA1003.
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; Beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=63699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-22491 / SEROTYPE 4A;
 RX MEDLINE-20222556; PubMed-10761919;
 RA Parkhill J., Achtman W., James K.D., Bentley S.D., Churcher C.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holtroyd S.,
 RA Javels R., Leather S., Moule S., Mungall K., Quail M.A.,
 RA Rainehead M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrett B.G.;
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 meningitidis 22491."
 RL Nature 404:502-506(2000).
 DR EMBL: AL162754; CAB84272.1; -
 KM Transmembrane.
 SO SEQUENCE 471 AA; 50623 MW; 1E0A3A08B8F6F6CB CRC64;

Query Match 8.4%; Score 93; DB 2; Length 471;
 Best Local Similarity 19.4%; Pred. No. 7.7;
 Matches 42; Conservative 37; Mismatches 74; Indels 64; Gaps 9;
 OY 39 ALMLDLVGLL-----VVAL-----IADPYHLYPA----- 65
 DB 165 AAMMELAMGMSHLDRERKRTYFVLLGIAVCASIGIGLTVGSPNDIAAKALNLD 224
 OY 66 YGVV-MEVAVFLVTLVIVFNLYL-----QLHMKLVVMPPL-----VLIMFNISATV 113

DB 225 VGMKRLGLPMMLLILPMLLSLYLILAKPNLNEVEIKASIPWYLRVIALILFLATAA 284
 OY 114 LYTFACSAVDLSLGRTPYNOAAAFACIWMATYGSVAFSSYQANGVGSN-- 171
 DB 285 WIPSSKIKTAFGIS-----NPDVIALSAVAVVFGVA-----QKEVARNRD 328
 OY 172 -AATSQMAGYATCATAPSGAANAAGSOSRYTLAS 207
 DB 329 WGYLMFGGISLTLTKTSGASEALGQVAAVFGSA 365

RESULT 6
 O44986 PRELIMINARY; PRT; 610 AA.
 AC O44986:
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE K02F2.6 PROTEIN.
 GN K02F2.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE-94150718; PubMed-7906398;
 RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Faveille A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Spoat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Magg L., Goela D.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF043699; AAB97568.1; -
 DR INTERPRO: IPR000276; -
 DR PFM: PFM0001; 7tm_1.1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
 KM G-protein coupled receptor; Transmembrane; Glycoprotein.
 SO SEQUENCE 610 AA; 67762 MW; 57DB24D638566C21 CRC64;

Query Match 8.4%; Score 93; DB 5; Length 610;
 Best Local Similarity 22.8%; Pred. No. 9.6;
 Matches 42; Conservative 39; Mismatches 67; Indels 36; Gaps 10;
 OY 33 VSRRLGALMLQLVGLLWALLADPYHLYPAYG--W-VAFVAVFLVTLVFNLYLFEOL 84
 DB 89 LRSATLILSLALADLVGLVTLPSIANEVLDQYWGEGWCTIWLIDIMCTASTY 148
 OY 85 NLYLFLHMKLVVMP--WPLVIMINISATV--LYTFACSAVDL-----TSL 131

DB 149 NVAISIDRYIAIKPLNPLMTKFRACVTAIWMISGLICSPSFLASSIKKOTPC 208
QY 132 RGRIPNO-----RAASFFACVMAIYGSASFYSQAMRGVSNATSMAGCIATT 184
DB 209 RCT-PNMGRTYVVSASSSFYPMIYF---VFRTY---VAARATKSIYSGMMSV 260
QY 185 CATA 188
DB 261 TAAA 264

RESULT 7
Q9LK50 PRELIMINARY: PRT: 693 AA.
AC 09LK50: 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE ABC TRANSPORTER-LIKE PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety p1,
RT TAC and BAC clones."
RL DNA Res. 7:217-221(2000).
DR EMBL: AP000375; BAB01414.1;
SQ SEQUENCE 693 AA; 78940 MW; 48F87D87413209A2 CRC64;

Query Match 8.4%; Score 93; DB 10; Length 693;
Best Local Similarity 19.6%; Pred. No. 11;
Matches 32; Conservative 35; Mismatches 72; Indels 24; Gaps 4;

QY 32 FVRSRLGALMLQVLYGLVVALNDPYHLPAYGWVFAVFLMTYIVLNLFLQL 91
DB 440 FOKRLVOSLGVAVVGLMMKSKDTDEHLRDYGLMFYICIF-WTSSSLFGAYVFF- 496
QY 92 HMKLWVWPLVLMFNISATVLYTATLACSAVDLTS-----LGRTRPIYOR 140
DB 497 -----PFKKLYLVEKKAERYRLSYVYVCSLCDMAVHLYPTFEMIYFMAEFMRN 549

QY 141 AAASFACVMAIYGSASFYSQAMRGVSNATSMAGCIATT 183
DB 550 IPCEFLFVLTITLITAIT---SOGAGEFTGASVLSIKRGMATAS 589

RESULT 8
Q9K032 PRELIMINARY: PRT: 471 AA.
AC 09K032: 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE TRANSPORTER, NADCO FAMILY.
GN NMB0792.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MC58 / SEROGROUP B;

RX MEDLINE=20175755; PubMed=10710307;
RA Tetteijn H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Hatt D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Clecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Yamatevan J.,
RA Gill J., Scarlato V., Maignant V., Pizsa M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58".
RL Science 287:1809-1815(2000).
DR EMBL: AE002433; AAF41205.1;
DR TIGR; NMB0792;
SQ SEQUENCE 471 AA; 50647 MW; 2DBC53ECC5ICE04 CRC64;

Query Match 8.4%; Score 92; DB 2; Length 471;
Best Local Similarity 19.4%; Pred. No. 9.2;
Matches 42; Conservative 37; Mismatches 74; Indels 64; Gaps 9;

QY 39 ALMLQVLYGLL-----VMAL-----IADPYHLVPA----- 65
DB 165 AAMMLPLMGMHSHDQKEKHETVYLLGLIYCASIGSIGTGLVSPPLIAKALNLD 224
QY 66 YGVV-MEFAVFLMLVTVLFLNLYL-----QLMKLWVWPL-----VLNFINISATV 113
DB 225 VGMKMLGIPMMLLILPLMLLSLYLILKPNLNERVEIKESIFMTLRYTALLIFLATAA 284
QY 114 LYTFATFACSAVDLTSRGRTPYNGRAASFACVMAIYGSASFYSQAMRGVSN-- 171
DB 285 WIFSSKITAFGIS-----NPDVIALSAVAAYVFGVA-----QMKVARNRD 328

QY 172 -AATSQMAGYATTCATAPSGAAGAAQSGSRVTLQAS 207
DB 329 GGVLMFLFGGISLSTLTKTSGNSALGQGVATFSGA 365

RESULT 9
Q21228 PRELIMINARY: PRT: 208 AA.
AC 021228: 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE 01-JAN-1999 (TREMblrel. 09, Last annotation update)
DE K04G2.9 PROTEIN.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Gardner A.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightling J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Hieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weissstock L., Wilkinson-Sprott J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans".
RL Nature 368:32-38(1994).
DR EMBL: Z75712; CAB00046.1;
SQ SEQUENCE 208 AA; 23669 MW; 4EB921774853A61F CRC64;

Query Match	8.38;	Score 91;	DB 5;	Length 208;
Best Local Similarity	24.68;	Pred. NO. 5.4;		
Matches	45;	Conservative	30;	Mismatches 76;
				Indels 32;
				Gaps 8

[illegible]

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RESULT 10
09K1T9
ID 09K1T9 PRELIMINARY; PRT; 379 AA.
AC 09K1T9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CELL SHAPE-DETERMINING PROTEIN MRDS.
GN CP1002.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_Taxid=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=1068435;
RA Reed T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T.,
RA Berry K., Bae S., Linher K., Weidman J., Khouri H., Craven B.,
RA Bowman C., Dodson R., Gwinn M., Nelson W., Debby R., Kolonay
RA McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis Mogen and Chlamydia
pneumoniae AR39."
RL Nucleic Acids Res. 28:1397-1406(2000).
DR EMBL; AE002257; AAF38780.1; -
CC TIGR; CP1002; -
SO SEQUENCE 379 AA; 42445 MF; 424DB4D23317F1AF CRC64;

```

[illegible]

Q0 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ROD SHAPE PROTEIN.
GN RODA.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxId=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CML029;
RX MEDLINE=99206606; PubMed=10192386;
RA Kaiman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Q138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shihai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CML029 from USA";
RL Nucleic Acids Res. 28:2311-2314(2000).
DR EMBL; AE001667; AAD15005.1; -
DR EMBL; AP002548; BAA99075.1; -
DR INTERPRO; IPR000255; -
DR INTERPRO; IPR001182; -
DR PFAM; PF01098; FTSW_RODA_SPOVE; 1.
DR PROSITE; PS00012; PHOSPHOTANTHETINE; UNKNOWN_1.
DR PROSITE; PS00428; FTSW_RODA_SPOVE; UNKNOWN_1.
SQ SEQUENCE 415 AA; 46662 MW; 2322206F5A6B9C CRC64;

[illegible]

RESULT	12		
068480		PRELIMINARY;	PRT; 273 AA.
ID	068480		
AC	068480;		
DT	01-AUG-1998	(Tremblrel, 07, Created)	
DT	01-AUG-1998	(Tremblrel, 07, Last sequence update)	
DT	01-MAY-1999	(Tremblrel, 10, Last annotation update)	
DE	ACCESSORY PROTEIN NOSY PRECURSOR.		
GN	NOSY.		
OS	Achromobacter cycloclastes.		
OC	Bacteriia; Proteobacteriia; beta subdivision; Alcaligenaceae;		
OC	Acetivibacter.		
OX	NCBI_TaxID=223;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-ATCC 21921, IAM 1013;		
RA	McGuire M.A., Nelson L.R., Bollinger J.A., Chan Y.-K., Dooley D.M.,		
RL	J. Inorg. Biochem. 0:0-0(1996).		
RP	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-IAM 1013;		

RX MEDLINE-99156231; PubMed-10048486;
 RA Inatomi K.;
 RT Analysis of the nitrous oxide reduction genes, nosZDYL, of
 RT Achromobacter cycloclastes.;
 RL DNA Ref. 5:365-371(1998).
 DR EMBL; AF047429; RAD09160.1;
 DR EMBL; Y15161; CAA75428.1;
 KW Signal.
 FT SIGNAL 273 273 POTENTIAL.
 SQ SEQUENCE 273 AA; 27648 MW; 1CDAB572876E28ID CRC64;

Query Match 8.2%; Score 90.5; DB 2; Length 273;
 Best Local Similarity 30.8%; Pred. No. 7.4; Mismatches 56; Indels 33; Gaps 7;
 Matches 49; Conservative 19;

OY 21 ASVSALRPDLGFEVRSRIGALMLQVLLGLVWALLADPPYHLV-----AYGWMFVA 73
 DB 123 ALAAVWFPDPG-ATNGLGLMLRL-IMSSVLGATFLGTCYALSALARRSGAAG-----LA 176
 OY 74 VELMTVTVLENYLYEQL-----HMKLYMPWPLY-----LMFINISATVLYTAFI 120
 DB 177 VALMTVAVLYLDALALALVTDGGNFTTHALPALLANPADAFREYFNLSAAQ----- 229
 OY 121 ACSAAVDLTSLRGTRPYNORAAAFACLYMAYGVSAF 159
 DB 230 AVSAGGLGGAAGTTPWOSASLAMPALAAALAAAF 268

RESULT 13
 OY 09M100 PRELIMINARY; PRT; 461 AA.

AC 09M100; 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE PUTATIVE SUGAR TRANSPORTER.
 GN AT4604750
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lamer B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL161501; CAB80840.1; -
 KW Sugar transport.
 SQ SEQUENCE 461 AA; 49470 MW; 652408EDD93DA3CA CRC64;

Query Match 8.2%; Score 90.5; DB 10; Length 461;
 Best Local Similarity 22.9%; Pred. No. 12;
 Matches 46; Conservative 28; Mismatches 62; Indels 65; Gaps 10;
 OY 1 MAE-----FBSKSTRSSPQAG-----AEASVSLARP-----DLGFVSRGAL 40
 DB 1 MAEESILPHEHTDVASPKRSSLSLSEISNASTRPFLAFVSGCALSFCICISFFGSI 60
 OY 41 MLQVLLGLVWALLADPPYHLVLYPGWMPFAVEL-RLVTVLENYLFLQHKML----- 95
 DB 61 LTVGLLGLLIGKRLADLVGRYTT--WITNVLVIGWLAFAFADVALLDGLRLGIGIS 118
 OY 96 -----YMPWPLVLMIFNISATVLYTAFIACSAVDLTSLRGTRPYNORAAAFACLY 150
 DB 119 VGSSVYLP-----YISEL-----APRLRGAASSIMQL- 148

OY 151 MIAGVSAFEESY---QAMGV 168
 DB 149 FVGVLSAFYALGTAIVAMRSL 169

RESULT 14
 OY 040568 PRELIMINARY; PRT; 401 AA.

AC 040568; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE PHOSPHATE TRANSLATOR PRECURSOR.
 OS Nicotiana tabacum (common tobacco).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=LEAF;
 RC MEDLINE-94166771; PubMed-8121415;
 RA Knight J.S., Gray J.C.;
 RT "Expression of genes encoding the tobacco chloroplast phosphate
 RT translocator is not light-regulated and is repressed by sucrose."
 RL Mol. Gen. Genet. 242:386-594(1994).
 DR EMBL; X75088; CAA52979.1; -
 DR MENDEL; 9334; Nicta;1243;9334.
 KW Signal.
 FT SIGNAL 1 73 POTENTIAL.
 FT CHAIN 74 401 PHOSPHATE TRANSLATOR.
 SQ SEQUENCE 401 AA; 43705 MW; 36CC65B59A945035 CRC64;

Query Match 8.2%; Score 90; DB 10; Length 401;
 Best Local Similarity 22.2%; Pred. No. 11;
 Matches 48; Conservative 31; Mismatches 73; Indels 64; Gaps 10;

OY 10 TRTSSPAGAAVSALRPDLGFEVRSRIGALMLQVLLGLVWALLADPPYHLVPGWV 69
 DB 72 TAASSPAGSDSAGDA-----KVGFFNKATLNGFF----- 102
 OY 70 MEVAVELMTVTVLENYLYEQLHKMLY-MVMPPLVLMIFNISATVLYI-----TAFIACSA 124
 DB 103 -----FEMWFLNVLFINI-----LNKRTYMPYPPYVSVIHLAVGVYCLISWTGLPRA 154
 OY 125 AVDLTSLRGTRPY-----NORAAAFACLYMAYGVSA-----FFSYQAMRGVSNAT 174
 DB 155 PIDSTQLKLLPVAFCALGHVTSVNSFAVAVSTHTIKALEPF-----NASA 204
 OY 175 SQMAGYATTCATAPSGAAG--SQSRVT-LOASW 208
 DB 205 SQFLLGQIIPALMLSLAPVVLGVSMASLTLSFWM 240

RESULT 15
 OY 045577 PRELIMINARY; PRT; 539 AA.

AC 045577; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE YBEC PROTEIN (ORF3).
 GN YBEC.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=168;
 RX MEDLINE-98044033; PubMed-9384377;
 Kunt F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.M., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.J., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Ertan K.D., Errington J., Fabret C., Ferrati E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizi A., Galleron N.,
 RA Ghm S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Halbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Kleier-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
 RA Paro V., Pohl T.M., Portetelle D., Portollik S., Prescott A.M.,
 RA Prescean E., Pujic P., Punnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivoita C., Rocha E., Roche B., Rose M., Sadale Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Yandenbol M., Vannier F., Vaasrotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipet A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the gram-positive bacterium Bacillus
 RT subtilis";
 RL Nature 390:249-256(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 526-539 FROM N.A.
 RC STRAIN-BR95;
 RX MEDLINE-94282317; PubMed-8012593;
 RA Nilsson R.P., Belier L., Ruderberg B.;
 RT "The glpT and glpQ genes of the glycerol regulon in Bacillus
 RT subtilis";
 RL Microbiology 140:723-730(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RA Haga K., Liu H., Yasumoto K., Takahashi H., Yoshikawa H.;
 RT "Sequence analysis of the 70kb region between 17 and 23 degree of the
 RT Bacillus subtilis chromosome";
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; 299105; CAB12006.1; -;
 DR EMBL; 226522; CAA81293.1; -;
 DR EMBL; AB006424; BAA33109.1; -;
 DR INTERPRO; IPR002027; -;
 DR INTERPRO; IPR002293; -;
 DR PFAM; PF00324; aa_permeases; 1.
 SQ SEQUENCE 539 AA; 59197 MW; 2D022FBI5CFA0610 CRC64;

Query Match 8.28; Score 90; DB 2; Length 539;
 Best Local Similarity 28.38; Pred. No. 15;
 Matches 39; Conservative 19; Mismatches 36; Indels 44; Gaps 9;
 QY 62 LYPAYGWMEFAVFLMTYIVLFNLKMLKLYMVPMPYLFNISATVLTAFIA 121
 Db 335 LHPITG-VPRQAMFNILVSRIF-LFLFR-----CGVLAELISVATLSYTF----- 380
 QY 122 CSAANDLTLRGT-----RP-----YNQRAAASF-FACLVM-----IAYGV 156
 Db 381 --GPIYVTLRRTGKDLVRLKGLNVIADLGFIFASLVLVYMAWPLTGLVLTLLGL 438
 QY 157 SAFSYQA---WRGVSN 171
 :| ||| | :| | |

Db 439 PLYFYQAKAKWKGGRN 456

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 Job time: 91 sec
